GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 06:11:13 ; Search time 6340.47 Seconds
(without alignments)
13027.239 Million cell updates/sec

Title: US-10-054-680-1
Perfect score: 2766
Sequence: 1 atggcgtggttaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2627.4	95.0	3186	11	BC036783	BC036783 Homo sapi
	2	1786.4	64.6	1788	29	AY401283	AY401283 Homo sapi
	3	1741.4	63.0	1788	29	AY401284	AY401284 Pan trogl
	4	1624.4	58.7	2534	11	AK044636	AK044636 Mus muscu
	5	1546.4	55.9	1788	29	AY401285	AY401285 Mus muscu
	6	1258.2	45.5	4374	11	AK035163	AK035163 Mus muscu
	7	1208.8	43.7	2922	29	AY398961	AY398961 Homo sapi
	8	1169.8	42.3	2922	29	AY398963	AY398963 Mus muscu
	9	1151.4	41.6	2516	29	AY408693	AY408693 Homo sapi
	10	978.4	35.4	2881	29	AY398962	AY398962 Pan trogl
	11	971	35.1	1589	11	CNSLT1IBJ	BX248763 human ful
	12	948.4	34.3	3573	11	AK048160	AK048160 Mus muscu
	13	899.6	32.5	941	13	BX374548	BX374548 BX374548
	14	874.8	31.6	2515	29	AY408695	AY408695 Mus muscu
	15	813.8	29.4	887	12	BI913344	BI913344 603178823
	16	768.2	27.8	939	13	BX347210	BX347210 BX347210
c	17	743.4	26.9	791	12	BI523145	BI523145 603175911
	18	739.8	26.7	792	12	BI522813	BI522813 603175911
	19	737.8	26.7	920	13	BX368185	BX368185 BX368185
	20	708.4	25.6	922	13	BX390204	BX390204 BX390204
	21	698.2	25.2	2472	29	AY408694	AY408694 Pan trogl
	22	673.2	24.3	775	13	BQ770745	BQ770745 UI-M-FI0-
	23	657	23.8	665	13	BQ189572	BQ189572 UI-E-EJ1-
	24	605.4	21.9	704	14	CF729293	CF729293 UI-M-HD0-
	25	598.6	21.6	971	13	BX368184	BX368184 BX368184
	26	574.6	20.8	752	14	CF532853	CF532853 UI-M-GH0-
	27	560.2	20.3	676	10	BB280958	BB280958 BB280958
c	28	553.6	20.0	1062	29	CNS04DXR	AL286344 Tetraodon
	29	516	18.7	527	12	BG910325	BG910325 602805921
	30	503.8	18.2	588	14	CF533347	CF533347 UI-M-FY0-
	31	483.2	17.5	854	13	BX325851	BX325851 BX325851
	32	480	17.4	1055	13	BU116565	BU116565 603138368
	33	452	16.3	717	13	BX501230	BX501230 DKFZp779K
	34	432	15.6	948	13	BU364393	BU364393 603585571
	35	422.8	15.3	684	13	BU363818	BU363818 603788721
	36	416.4	15.1	718	12	BI756778	BI756778 603024449
	37	412.4	14.9	503	28	BZ211245	BZ211245 CH230-426
	38	407.8	14.7	475	10	BF190598	BF190598 237175 MA
c	39	407.4	14.7	499	28	BH349372	BH349372 CH230-32M
	40	405	14.6	641	13	BX502588	BX502588 DKFZp779P
	41	397.2	14.4	911	13	BU901346	BU901346 AGENCOURT
	42	390.2	14.1	597	13	BX502589	BX502589 DKFZp779P
	43	376.8	13.6	694	13	BX854768	BX854768 BX854768
	44	372.8	13.5	3063	11	BC023215	BC023215 Homo sapi
	45	368.4	13.3	1201	13	BX355386	BX355386 BX355386

ALIGNMENTS

RESULT 1
BC036783
LOCUS BC036783 3186 bp mRNA linear HTC 19-NOV-2003
DEFINITION Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3, mRNA (cDNA clone IMAGE:5732743), with apparent retained intron.
ACCESSION BC036783
VERSION BC036783.1 GI:23331089
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3186)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 3186)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: j Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17865803
This clone has the following problem: retained intron.

FEATURES Location/Qualifiers
source 1. .3186
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5732743"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_124"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 95.0%; Score 2627.4; DB 11; Length 3186;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2628; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        558 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 617

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 677

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 737

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        738 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAG 797

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        798 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 857

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        858 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 917
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        978 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1037

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       1038 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1097

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db       1098 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1157

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1158 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1217

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1218 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1277

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1278 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1337

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       1818 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1877

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
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Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Db       3138 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAA 3186
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RESULT 2
AY401283
LOCUS       AY401283               1788 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401283
VERSION     AY401283.1  GI:39757272
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
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  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /locus_tag="HCM0839"
ORIGIN

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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1787;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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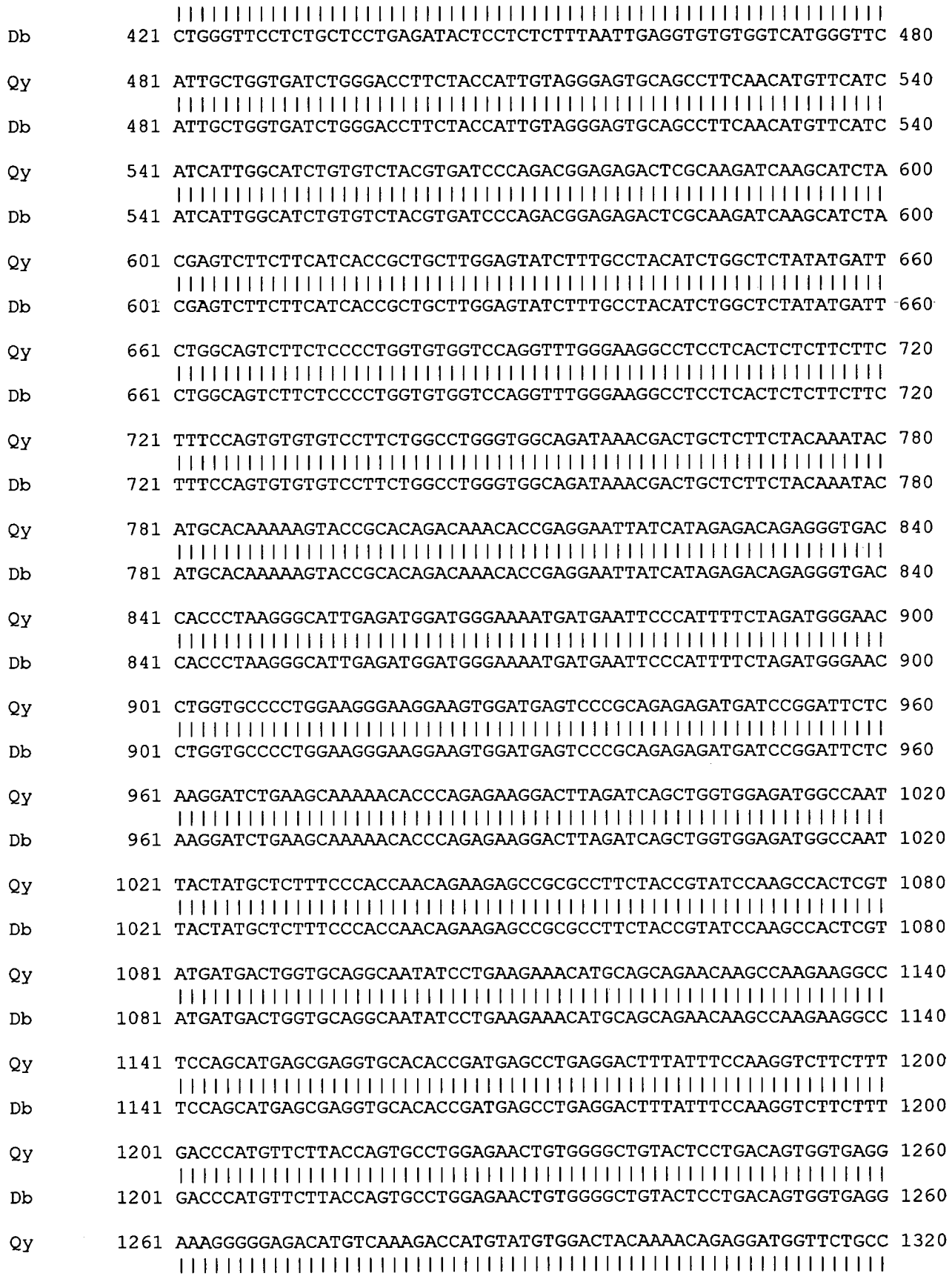

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LOCUS       AY401284                1788 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401284
VERSION     AY401284.1  GI:39757273
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1788)
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  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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     gene            <1. .>1788
                     /gene="SLC8A3"
                     /locus_tag="HCM0839"
ORIGIN

  Query Match             63.0%;  Score 1741.4;  DB 29;  Length 1788;
  Best Local Similarity   97.8%;  Pred. No. 0;
  Matches 1748;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db        781 ATGCACAAAAAGTACCGCACAGATAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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RESULT 4
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LOCUS       AK044636               2534 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus adult retina cDNA, RIKEN full-length enriched library,
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            exchanger), member 3, full insert sequence.
ACCESSION   AK044636
VERSION     AK044636.1  GI:26336660
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
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REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
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REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2534)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers

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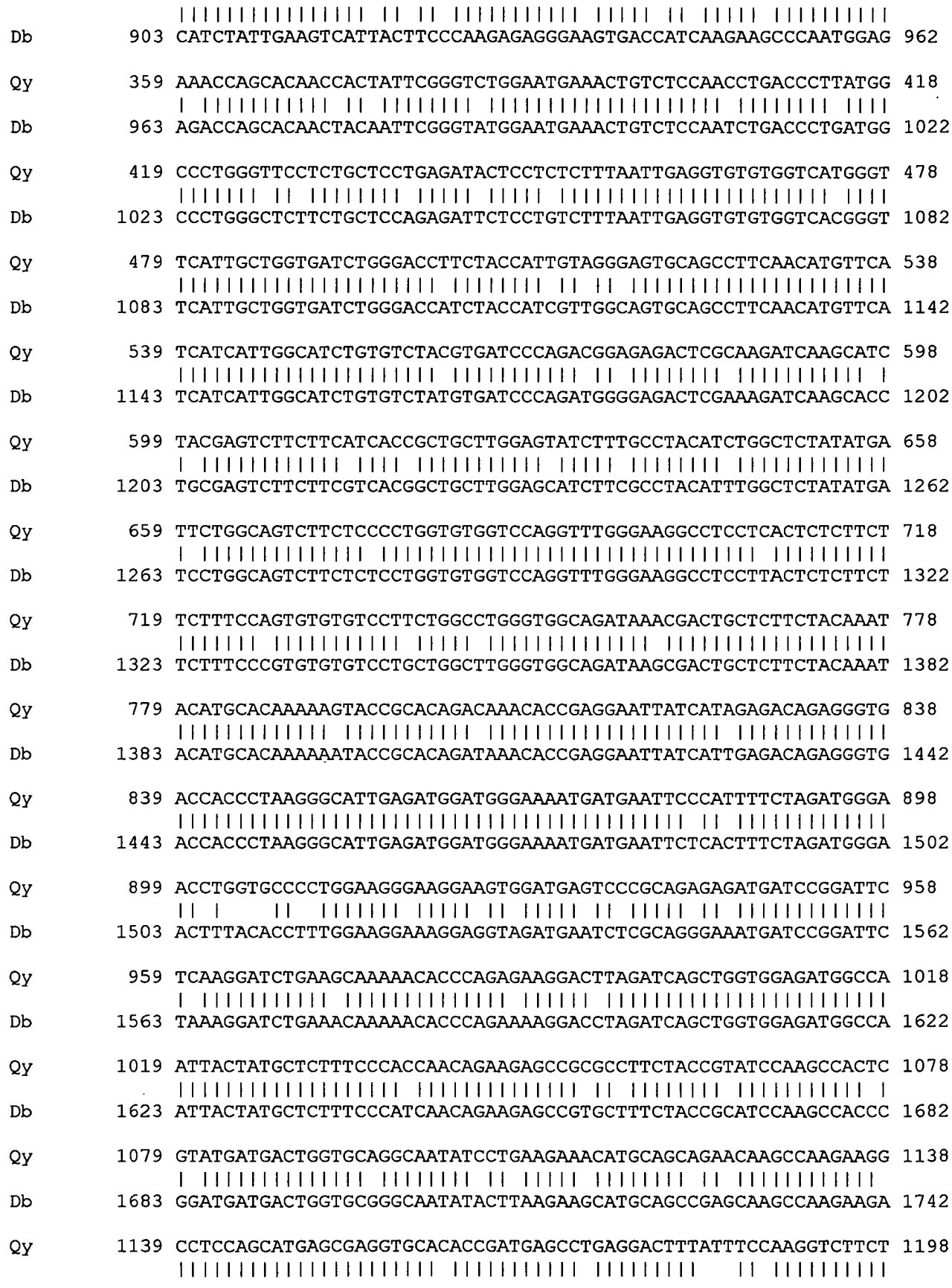

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RESULT 5
AY401285
LOCUS AY401285 1788 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY401285

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VERSION     AY401285.1  GI:39757274
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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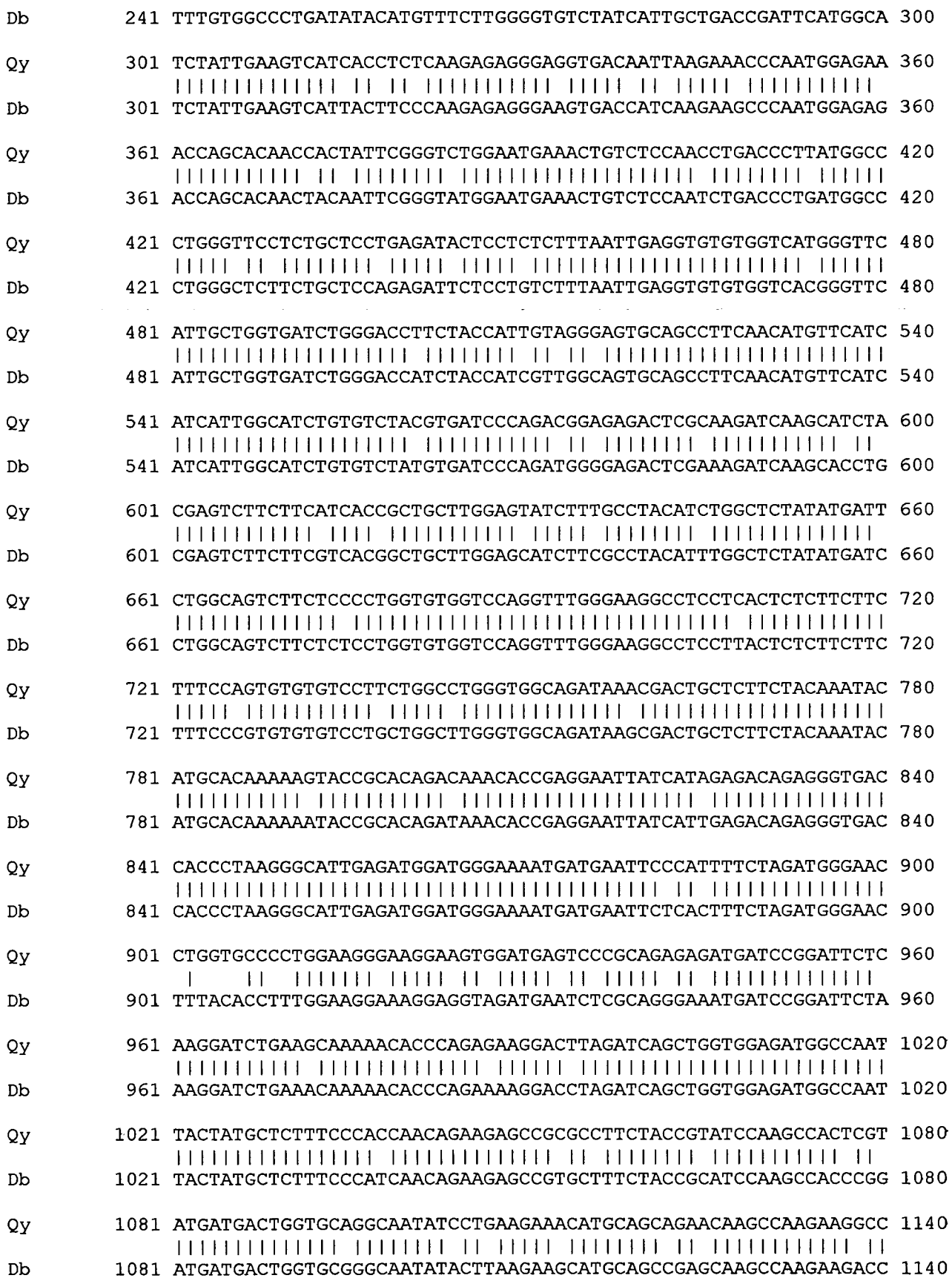

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RESULT 6
AK035163

LOCUS	AK035163 4374 bp mRNA linear HTC 18-SEP-2003
DEFINITION	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430095C22 product:SODIUM/CALCIUM EXCHANGER 2 PRECURSOR (NA(+)/CA(2+)-EXCHANGE PROTEIN 2) homolog [Rattus norvegicus], full insert sequence.
ACCESSION	AK035163
VERSION	AK035163.1 GI:26084435
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4374)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 45.5%; Score 1258.2; DB 11; Length 4374;
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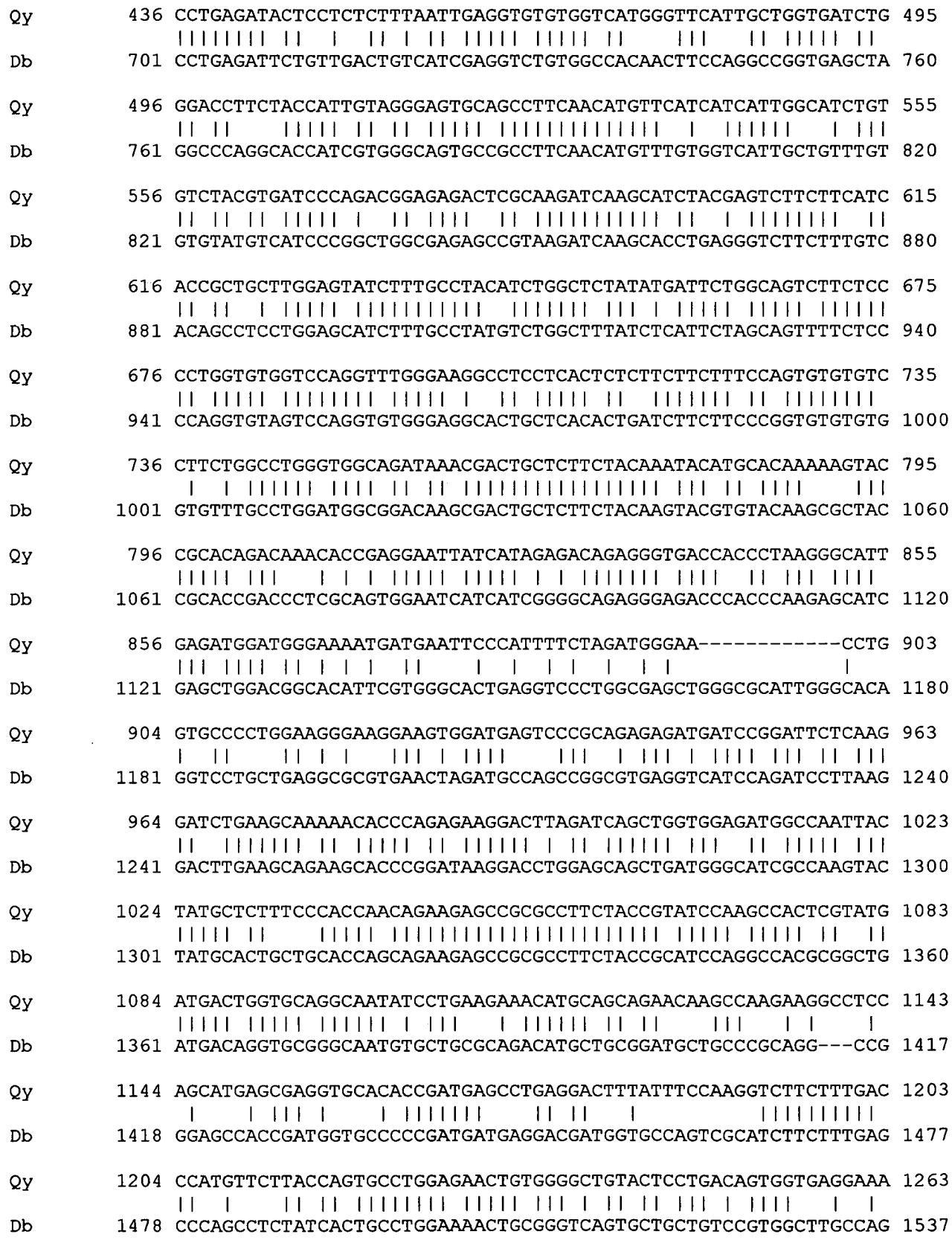

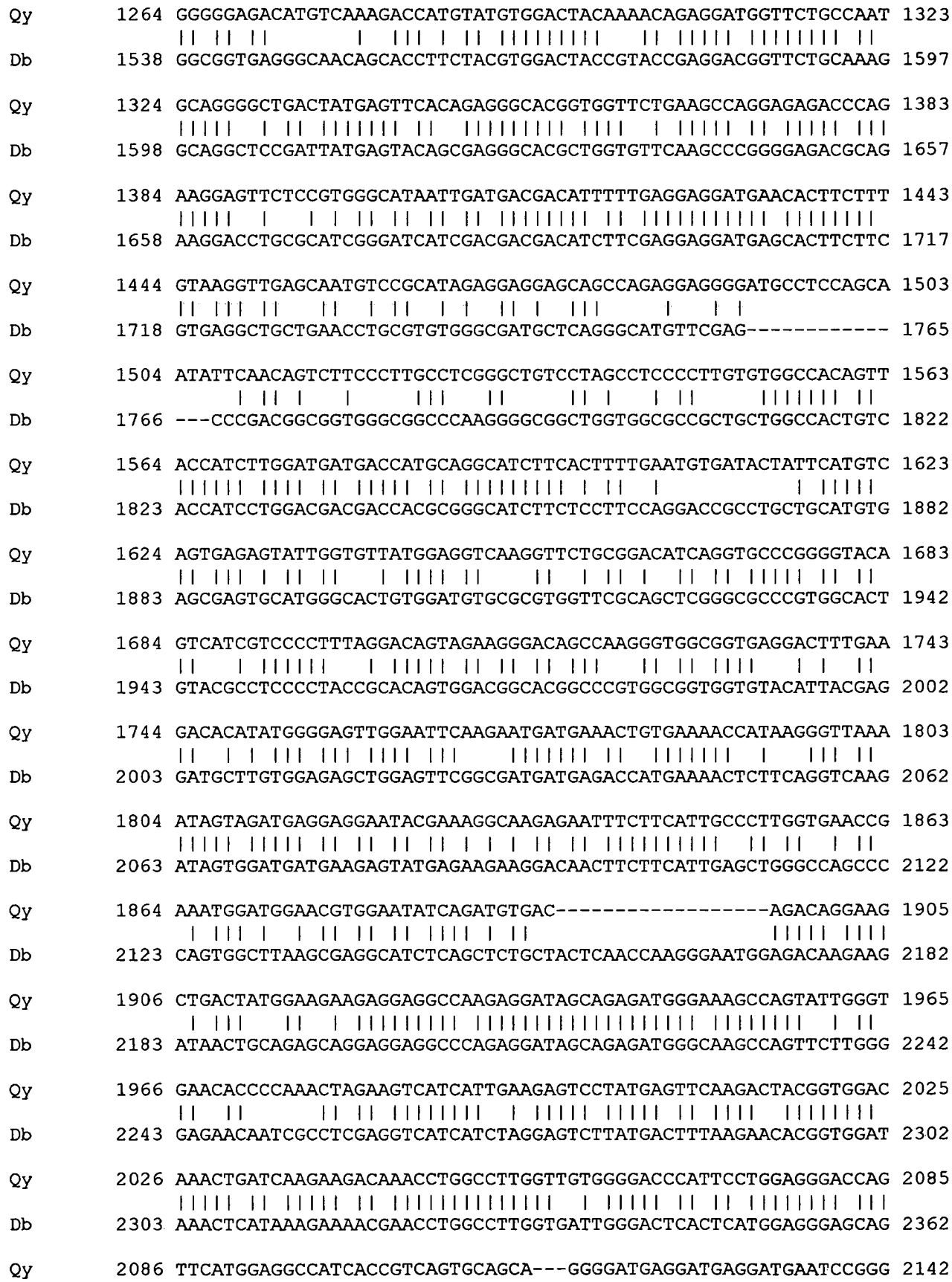

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Qy       2503 TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA 2562
              ||  |||||  ||  |  ||||||||  |||||||  |      |||  |  |||    ||  |||||
Db       2783 TCGGTGGCAGCGGTATACTGGGCGGTGCAGGGTCGCCCCTTCGAGGTGCGTGCAGGCACG 2842

Qy       2563 CTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG 2622
              ||||||||||||  |||||  ||  ||||||  ||||  ||  ||  ||  ||||||    |||||  |||
Db       2843 CTGGCCTTCTCGGTCACGCTGTTCACCGTCTTCGCCTTCGTGTGCATCGCAGTGCTGTTG 2902

Qy       2623 TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC 2682
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Db       2903 TACCGGCGCCGGCCGCAGATTGGCGGCGAGCTGGGCGGCCCGCGGGGACCCAAGCTGGCC 2962

Qy       2683 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2742
              ||  ||     |||||  ||  ||||  |||  ||||||||||  |||||  |||  ||  |||||
Db       2963 ACCACCGCTCTCTTCCTGGGCCTCTGGTTCCTCTACATTCTCTTCTCCAGCCTGGAGGCT 3022

Qy       2743 TATTGCTACATCAAGGGGTTCTA 2765
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Db       3023 TACTGCCACATCCGGGGCTTCTA 3045


RESULT 7
AY398961
LOCUS       AY398961               2922 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY398961
VERSION     AY398961.1  GI:39754950
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2922
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>2922
                     /gene="SLC8A1"
                     /locus_tag="HCM0065"
ORIGIN

  Query Match             43.7%;  Score 1208.8;  DB 29;  Length 2922;
  Best Local Similarity   66.9%;  Pred. No. 6e-286;
  Matches 1887;  Conservative    0;  Mismatches  762;  Indels  171;  Gaps    5;

Qy        109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
              ||  ||  | |   |||  |  | | ||     ||| | || ||||   |||| ||| |
Db        112 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 171

Qy        169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
              || || ||  |||| || ||| | ||  |  |||||||  |||||||||| ||||| ||
Db        172 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 231

Qy        229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
              |  | ||| ||||||||||||| || | |||||||| ||||| || || ||||| |||||
Db        232 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 291

Qy        289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
              || |||||| | ||||| |||||||||| |||||||| |  ||  | || || ||||||
Db        292 CGGTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA 351

Qy        349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408
              |||||||||| |||| ||  || ||| |  || |||||||||||| || || ||||||
Db        352 CCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 411

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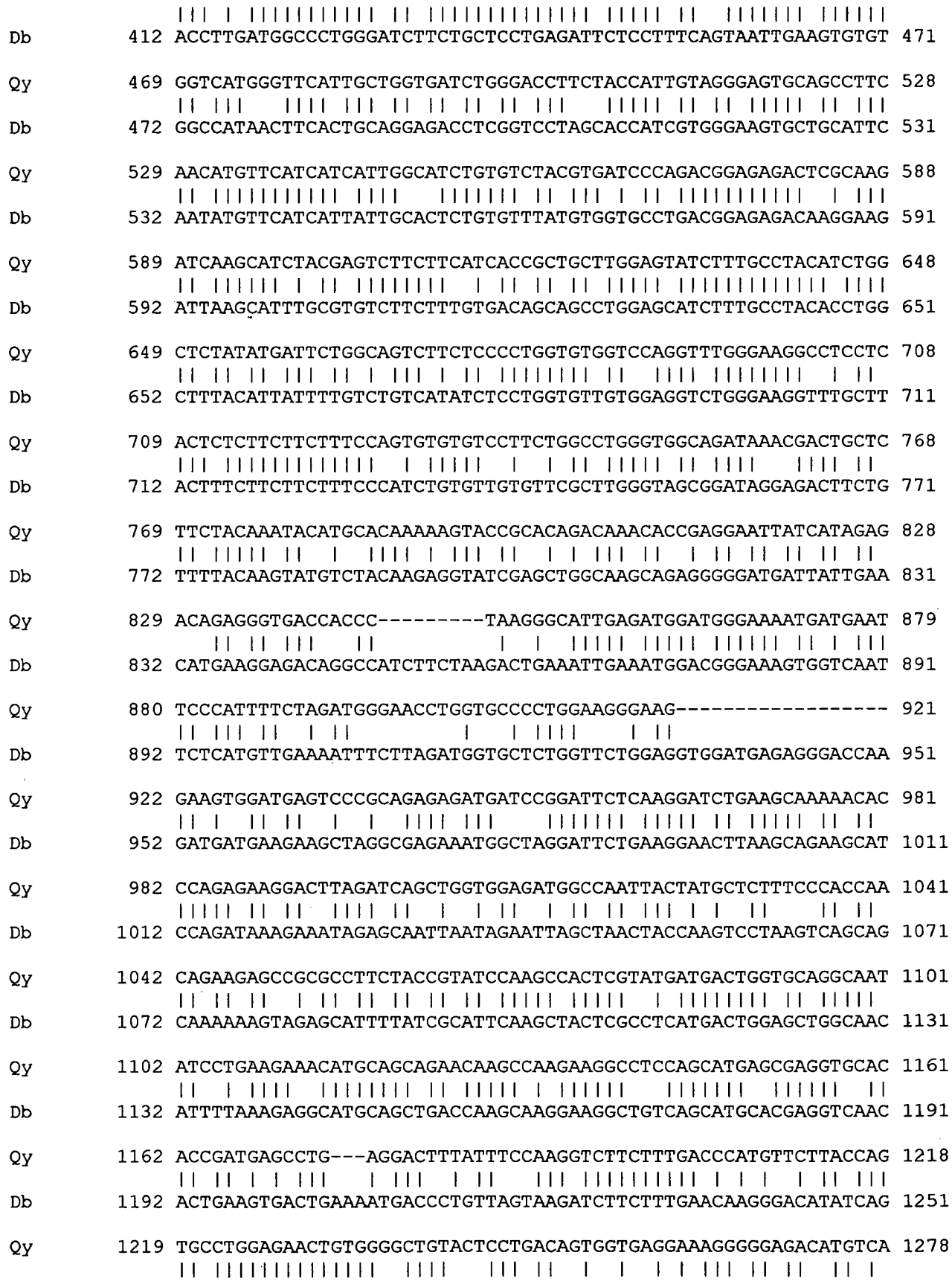

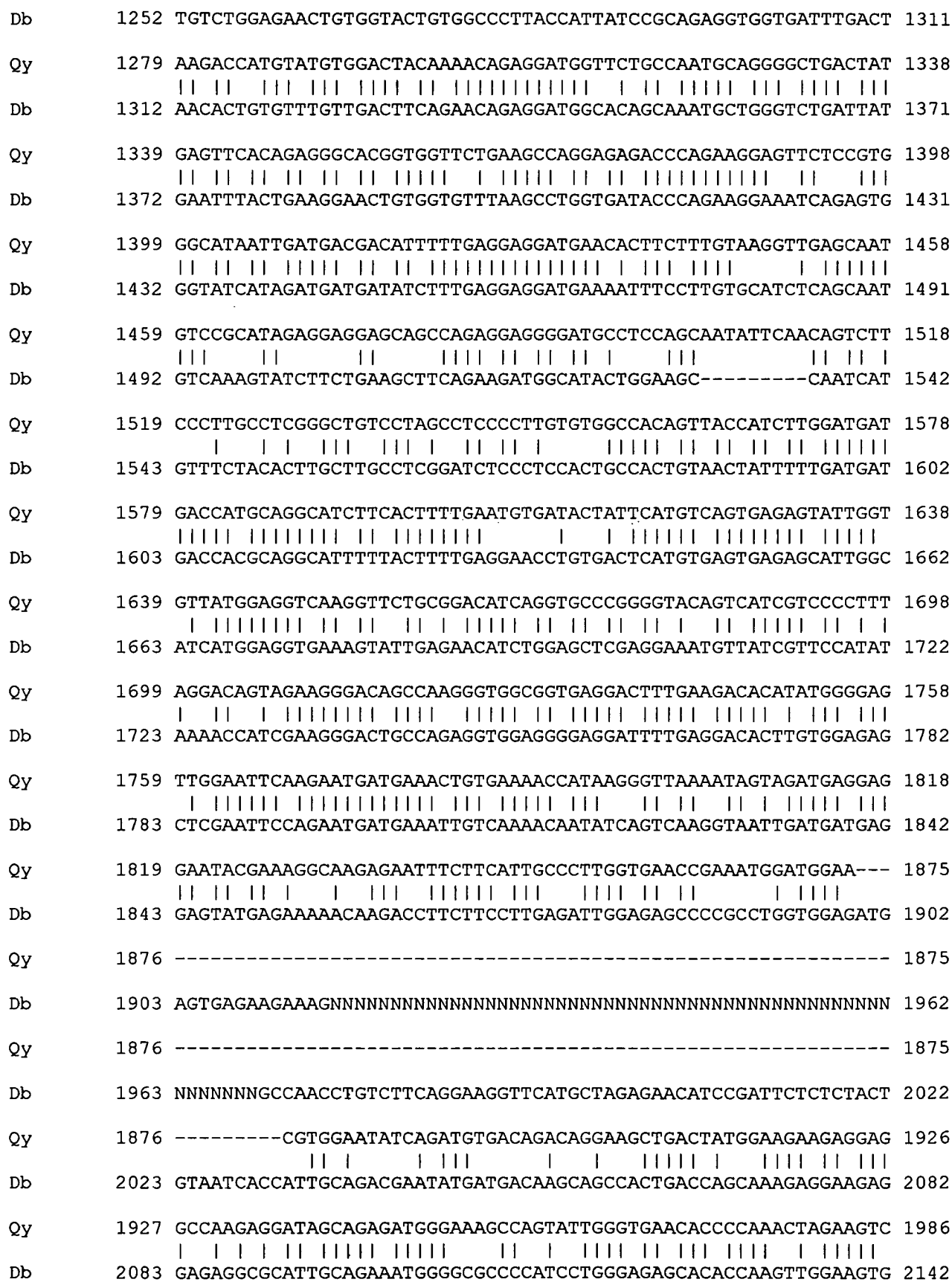

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Qy       1987 ATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAAC 2046
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Db       2143 ATCATTGAAGAATCCTATGAATTCAAGAGTACTGTGGACAAACTCATTAAGAAGACAAAC 2202

Qy       2047 CTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATCACCGTC 2106
             |||||| | || || |||||  |   |||||| || |||||||| || || ||||| |||
Db       2203 CTGGCCCTTGTGGTTGGGACTAACAGCTGGAGAGAACAGTTCATTGAAGCTATCACTGTC 2262

Qy       2107 AGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTT 2166
             ||||| |  | ||||| || || ||||||| ||||| |||| |||||||||||| ||
Db       2263 AGTGCTGGGGAAGATGATGACGACGATGAATGTGGGGAAGAGAAGCTGCCCTCCTGTTTC 2322

Qy       2167 GACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCC 2226
             || ||||| |||||||| |||||||| |||||||||| |||||||||  || |||||
Db       2323 GATTACGTGATGCACTTTCTGACTGTGTTCTGGAAGGTCCTGTTTGCCTTCGTCCCCCCT 2382

Qy       2227 ACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTC 2286
             || || |||||  | |||||||| || |||  |||||||||||||| |||||| | ||
Db       2383 ACTGAATACTGGAATGGCTGGGCGTGTTTCATTGTCTCCATCCTCATGATTGGCCTACTG 2442

Qy       2287 ACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCA 2346
             || ||  ||||||| |||||||| || ||||| |||||||||||||| || ||||||||
Db       2443 ACAGCTTTCATTGGAGACCTGGCTTCCCACTTTGGCTGCACCATTGGCCTGAAAGATTCT 2502

Qy       2347 GTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAA 2406
             || || || || || ||||| ||| |||| || || || ||||| || ||||||||||||
Db       2503 GTGACTGCAGTCGTGTTCGTCGCACTTGGAACATCAGTGCCAGACACATTTGCCAGCAAA 2562

Qy       2407 GCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAAC 2466
             |  || |||  ||||||    |||||||||||||||| || ||||| ||||||||||||
Db       2563 GTGGCAGCCACCCAGGACCAGTATGCAGACGCCTCCATAGGTAACGTCACGGGCAGCAAC 2622

Qy       2467 GCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCT 2526
             || || |||||||||||||| |||||  |||||||||| | || |||||||||   ||
Db       2623 GCGGTGAATGTCTTCCTGGGAATCGGTGTGGCCTGGTCCATCGCTGCCATCTACCACGCA 2682

Qy       2527 CTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTC 2586
                 | ||  |  ||||| | |||||  | |||||||| || ||||| ||||| ||||||
Db       2683 GCCAATGGGGAACAGTTCAAAGTGTCCCCTGGCACACTAGCTTTCTCTGTCACTCTCTTC 2742

Qy       2587 ACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGA 2646
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Db       2743 ACCATTTTTGCTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGAGGCCAGAAATCGGA 2802

Qy       2647 GGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTG 2706
             || ||||| ||||| |||||      |||||||  |||| | || |||||||||  |||
Db       2803 GGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTCTTTGTGCTCCTA 2862

Qy       2707 TGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTCTAA 2766
             |||||| | |||||  ||||  || | || |||||||| ||| |||| || || ||||||
Db       2863 TGGCTCTTGTACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATAAAAGGCTTCTAA 2922
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RESULT 8
AY398963
LOCUS AY398963 2922 bp DNA linear GSS 15-DEC-2003

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DEFINITION  Mus musculus SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY398963
VERSION     AY398963.1  GI:39754952
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /locus_tag="HCM0065"
ORIGIN
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  Matches 1845;  Conservative    0;  Mismatches  771;  Indels  171;  Gaps    5;

Qy        142 TGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAAC 201
              ||| | || ||||   |||| ||| | || || ||| |||| || ||| | ||  |  ||
Db        145 TGTACTGGCTCATATTACTGTAAGAAAGGGGTGATCTTGCCCATTTGGGAACCCCAAGAC 204

Qy        202 CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG 261
              || ||  |||||||||| ||||| || |  | ||| |||||||||||| || | ||||||
Db        205 CCATCTTTTGGGGACAAAATTGCTAGAGCAACTGTGTATTTTGTGGCCATGGTCTACATG 264

Qy        262 TTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT 321
              |||||||| || || || ||||| ||||| || ||| | ||||| || ||||||||||||
Db        265 TTCCTTGGAGTTTCTATTATTGCAGACCGGTTTATGTCCTCTATAGAGGTCATCACCTCT 324

Qy        322 CAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGG 381
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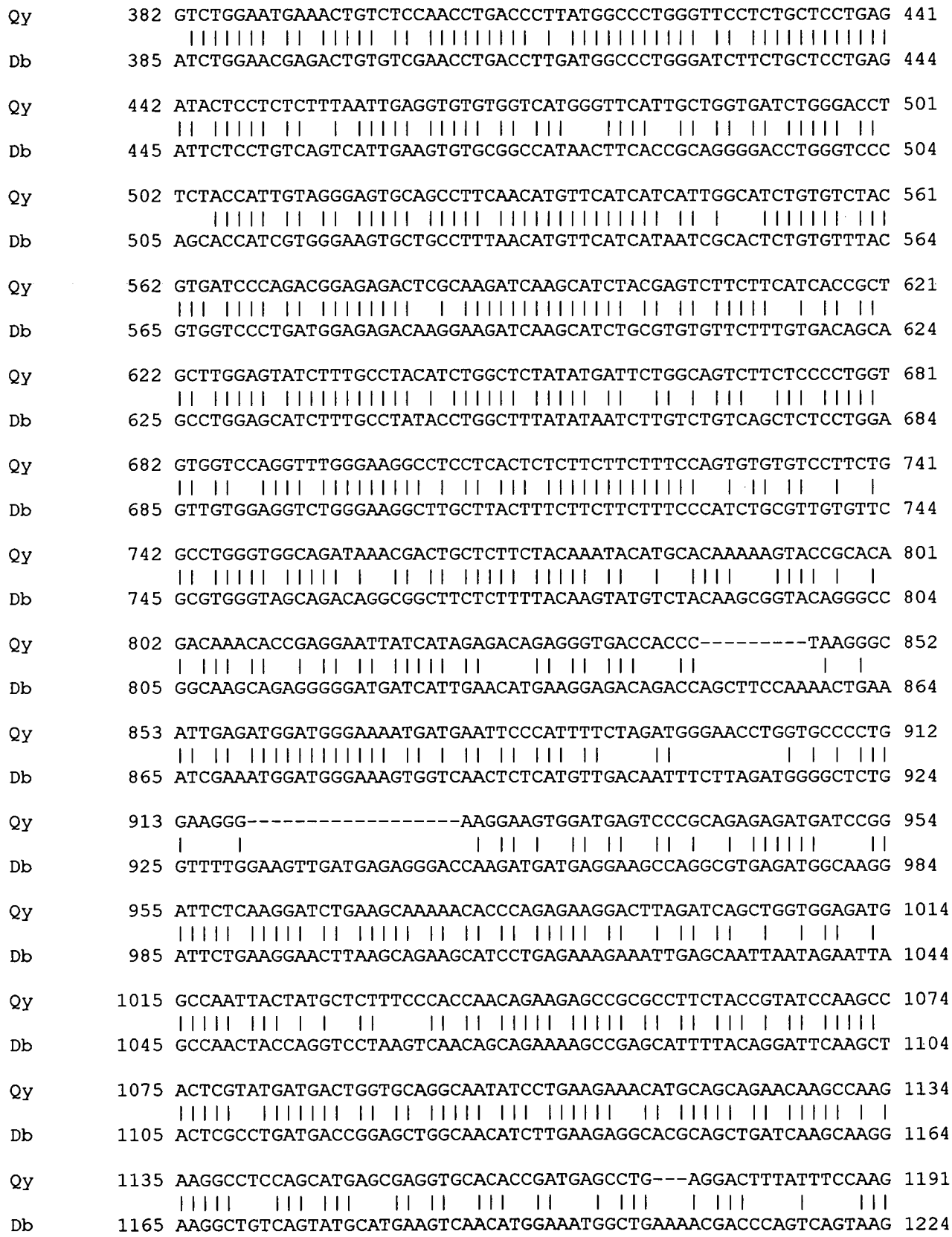

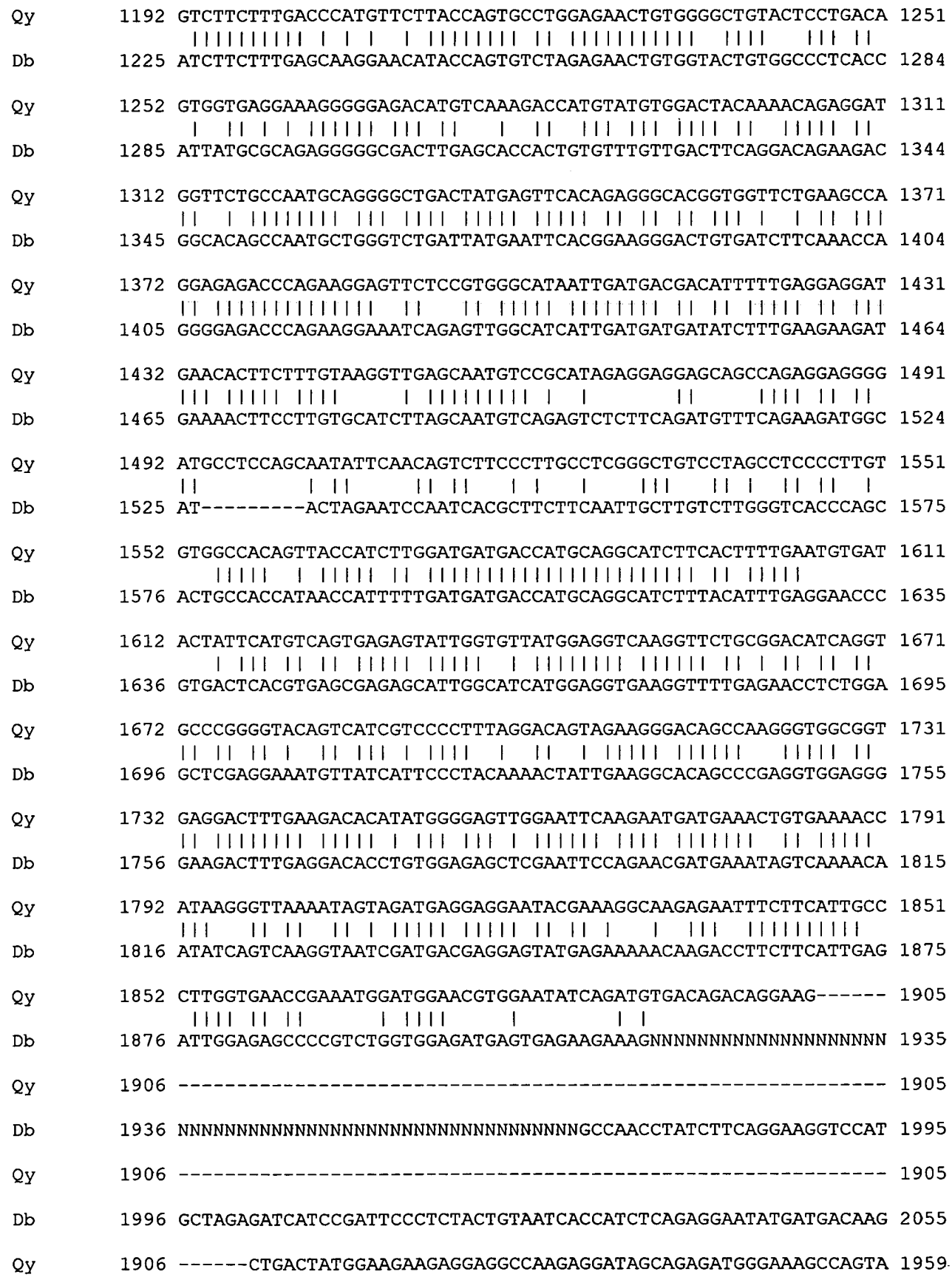

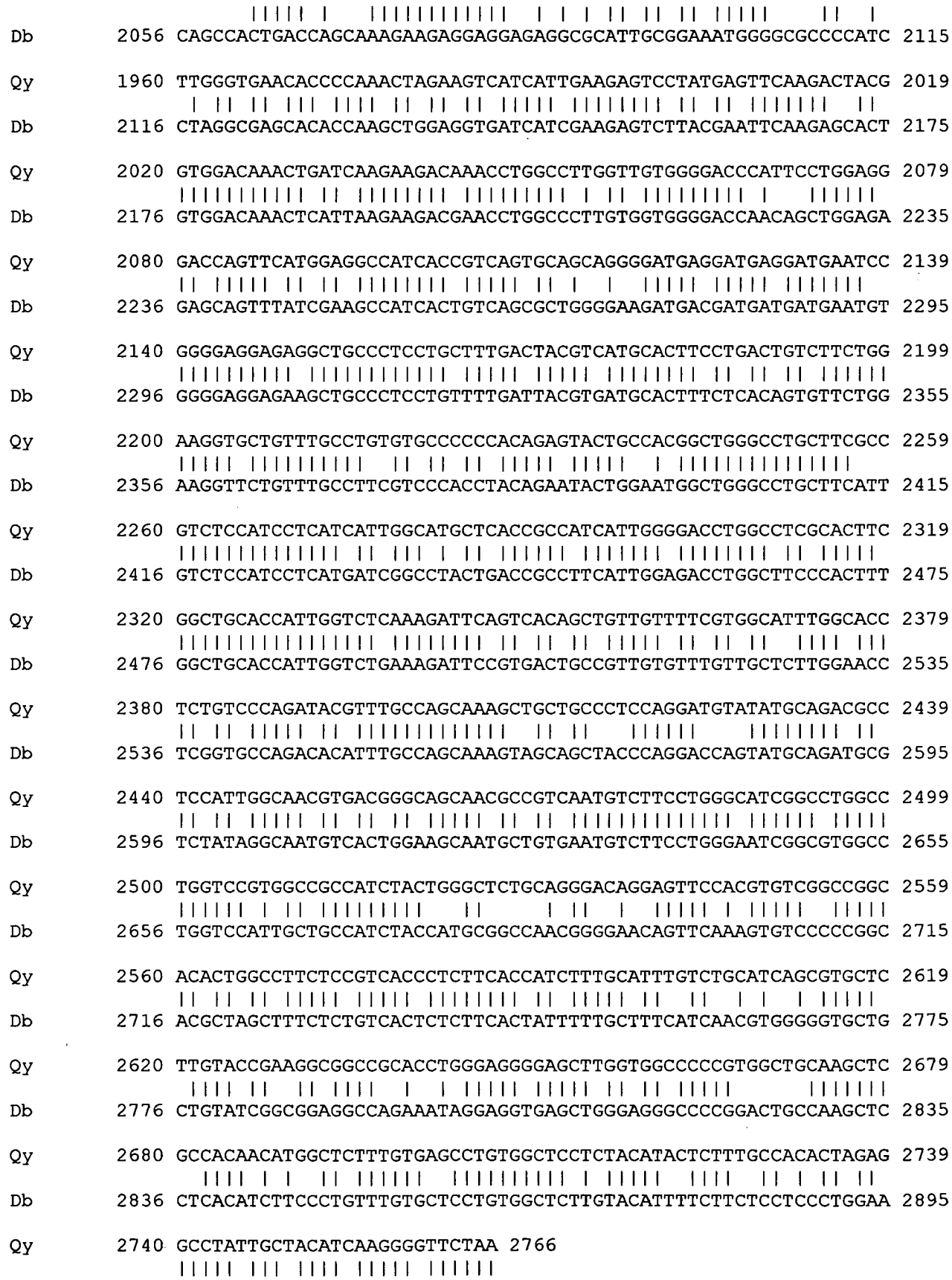

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Db       2896 GCCTACTGCCACATAAAGGGCTTCTAA 2922


RESULT 9
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LOCUS       AY408693                2516 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM3309 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY408693
VERSION     AY408693.1  GI:39764664
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2516)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2516)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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  Matches 1673;  Conservative    0;  Mismatches  809;  Indels   51;  Gaps    5;

Qy        266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
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Qy        326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 385
              ||| |||| | || || |  ||  |||| || || ||||||     |||  ||||  |||
Db         61 AGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTGGGCACCGTTCGCATCT 120

Qy        386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 445
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Db        121 GGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCCTCCGCACCTGAGATCC 180

Qy        446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 505

Db        181 TGCTGTCAGTCATCGAAGTCTGCGGCCACAACTTCCAGGCGGGTGAGCTGGGCCCAGGCA 240

Qy        506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 565

Db        241 CCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCCGTGTGCATCTACGTCA 300

Qy        566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625

Db        301 TCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTCTTTGTCACTGCCTCTT 360

Qy        626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685

Db        361 GGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTTTTTTCCCCCGGTGTGG 420

Qy        686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745

Db        421 TCCAGGTGTGGGAGGCGCTGCTGACCCTGGTCTTCTTCCCGGTGTGCGTGGTATTCGCCT 480

Qy        746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805

Db        481 GGATGGCCGACAAGCGGCTGCTCTTCTACAAGTACGTGTACAAGCGCTACCGCACCGACC 540

Qy        806 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 865

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Qy        866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAA----------CCTGGTGCCCCTGG 913

Db        601 GCACGTTCGTGGGCGCCGAGGCCCCAGGTGAGCTGGGCGGCCTGGGCCCGGGCCCCGCCG 660

Qy        914 AAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGC 973

Db        661 AGGCGCGCGAGCTGGACGCCAGCCGCCGCGAGGTCATCCAGATCCTCAAGGACCTCAAGC 720

Qy        974 AAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTT 1033

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Qy       1034 CCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTG 1093

Db        781 TGCACCAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACGCGGCTGATGACCGGCG 840

Qy       1094 CAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCG 1153

Db        841 CCGGGAACGTGCTGCGCAGACACGCGGCGGACGCCTCGCGCAGGGCGGC---GCCGGCCG 897

Qy       1154 AGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTT 1213

Db        898 AGGGCGCGGGCGAGGACGAAGACGACGGCGCCAGCCGCATCTTCTTCGAGCCTAGCCTCT 957

Qy       1214 ACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACA 1273

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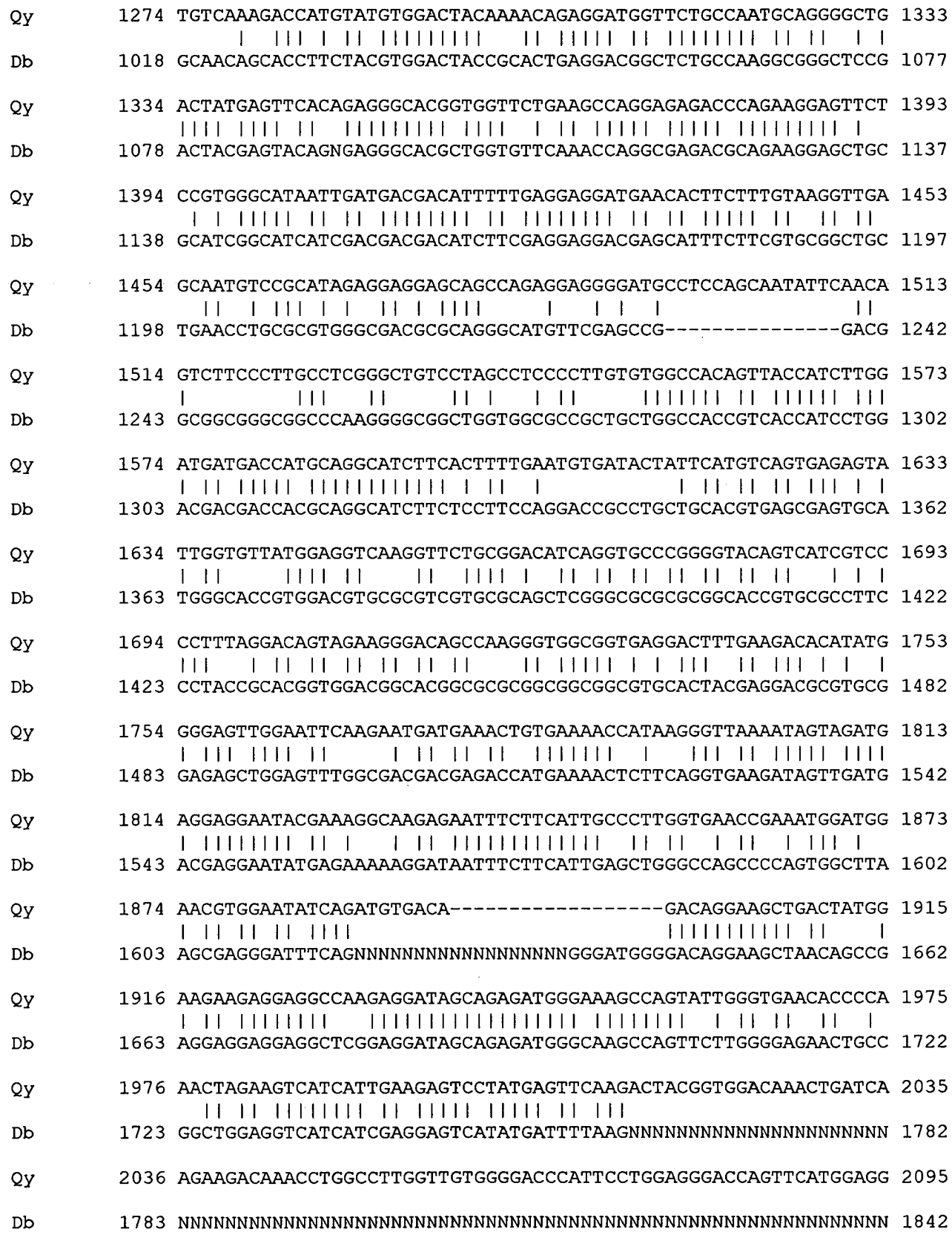

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Qy       2153 TGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTG 2212
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Qy       2213 CCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCA 2272
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Qy       2273 TCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTG 2332
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Qy       2333 GTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATA 2392
              | ||||| || || |||| |||||||| ||||| ||  | ||||||||  |||| || |
Db       2083 GCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGCACCTCCATCCCTGACA 2142

Qy       2393 CGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACG 2452
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Db       2143 CGTTCGCCAGCAAGGTGGCGGCGCTGCAGGACCAGTGCGCCGACGCGTCCATCGGCAACG 2202

Qy       2453 TGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCG 2512
              |||| |||  |||||| || || || ||||| ||| | ||| | |||||||| |||||||
Db       2203 TGACCGGCTCCAACGCGGTGAACGTGTTCCTTGGCCTGGGCGTCGCCTGGTCTGTGGCCG 2262

Qy       2513 CCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCT 2572
              || | ||||||||  ||||||| |     ||| | |||    | ||||| ||||||||||
Db       2263 CCGTGTACTGGGCGGTGCAGGGCCGCCCCTTCGAGGTGCGCACTGGCACGCTGGCCTTCT 2322

Qy       2573 CCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGC 2632
              ||||||| ||||||||| |||| || || ||  ||||   ||||||  |||||||  | |
Db       2323 CCGTCACGCTCTTCACCGTCTTCGCCTTCGTGGGCATTGCCGTGCTGCTGTACCGGCGCC 2382

Qy       2633 GGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGC 2692
              |||||||| | || || ||||| || ||||| || ||   |||||||||||| ||   ||
Db       2383 GGCCGCACATCGGCGGCGAGCTGGGCGGCCCGCGCGGACCCAAGCTCGCCACCACCGCGC 2442

Qy       2693 TCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACA 2752
              ||||  || |||| |||||||| ||||| ||||| ||||  || ||||| || ||| |||
Db       2443 TCTTCCTGGGCCTCTGGCTCCTGTACATCCTCTTCGCCAGCCTGGAGGCGTACTGCCACA 2502

Qy       2753 TCAAGGGGTTCTA 2765
              ||  ||| |||||
Db       2503 TCCGGGGCTTCTA 2515
```

RESULT 10
AY398962
LOCUS AY398962 2881 bp DNA linear GSS 15-DEC-2003
DEFINITION Pan troglodytes SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY398962
VERSION AY398962.1 GI:39754951
KEYWORDS GSS.

```
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 2881)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2881)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2881
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>2881
                     /gene="SLC8A1"
                     /locus_tag="HCM0065"
ORIGIN

  Query Match             35.4%;  Score 978.4;  DB 29;  Length 2881;
  Best Local Similarity   56.4%;  Pred. No. 3.4e-229;
  Matches 1587;  Conservative    0;  Mismatches 1057;  Indels  171;  Gaps    5;

Qy        109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
              ||  ||  | |   |||  |  | | ||     ||| | || ||||   |||| ||| |
Db         76 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 135

Qy        169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
              || || ||  |||| || ||| | ||  |     ||||  |||||||||| |||||
Db        136 GGGGTGATTTTGCCCATTTGGGAACCCCANNNNNCTTCTTTTGGGGACAAAATTGCTNNN 195

Qy        229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
              |  | |||  |||||||||||| || | |||
Db        196 GCTACTGTGTATTTTGTGGCCATGGTCTACNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 255

Qy        289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348

Db        256 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 315

Qy        349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408

Db        316 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 375
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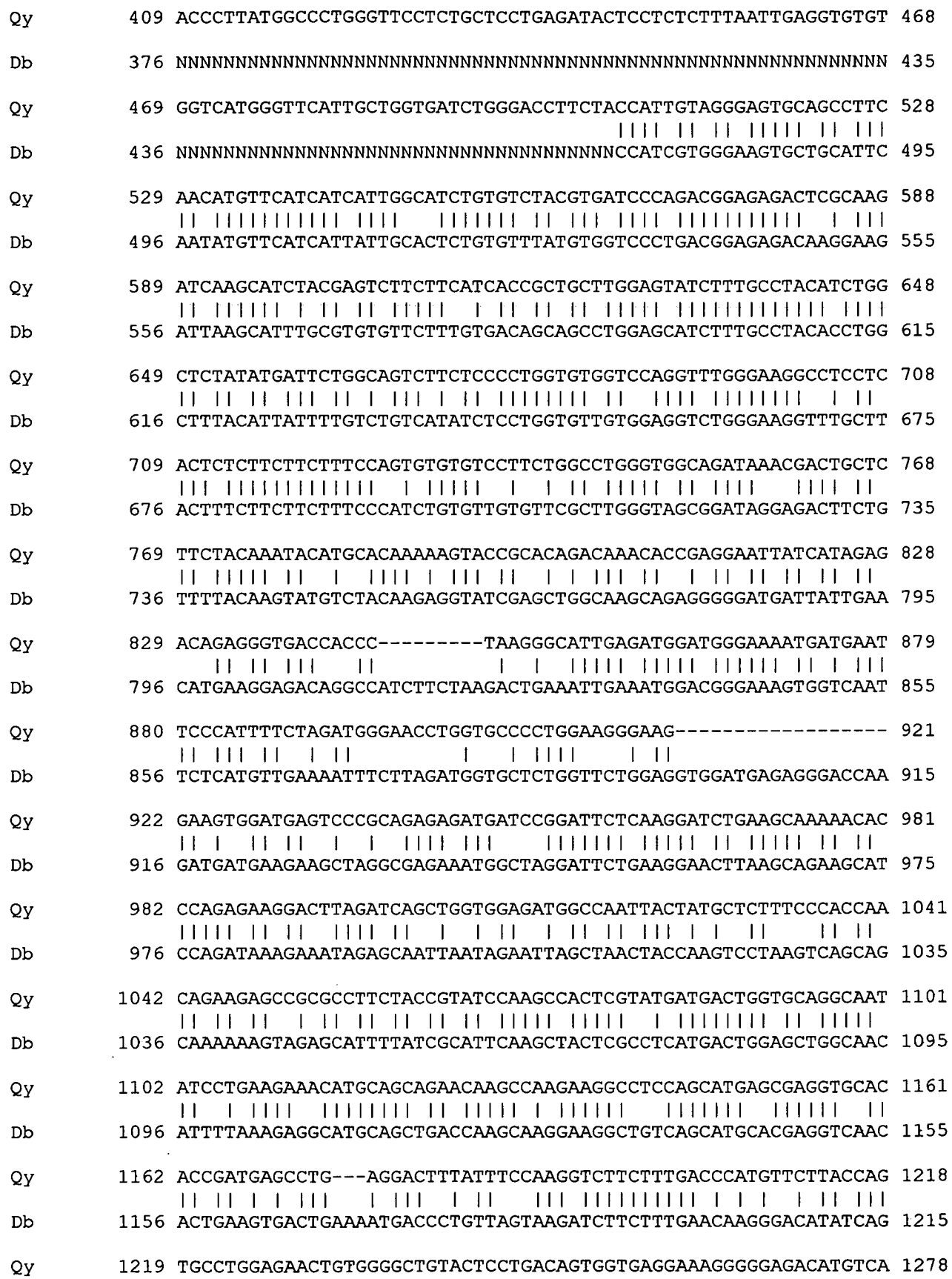

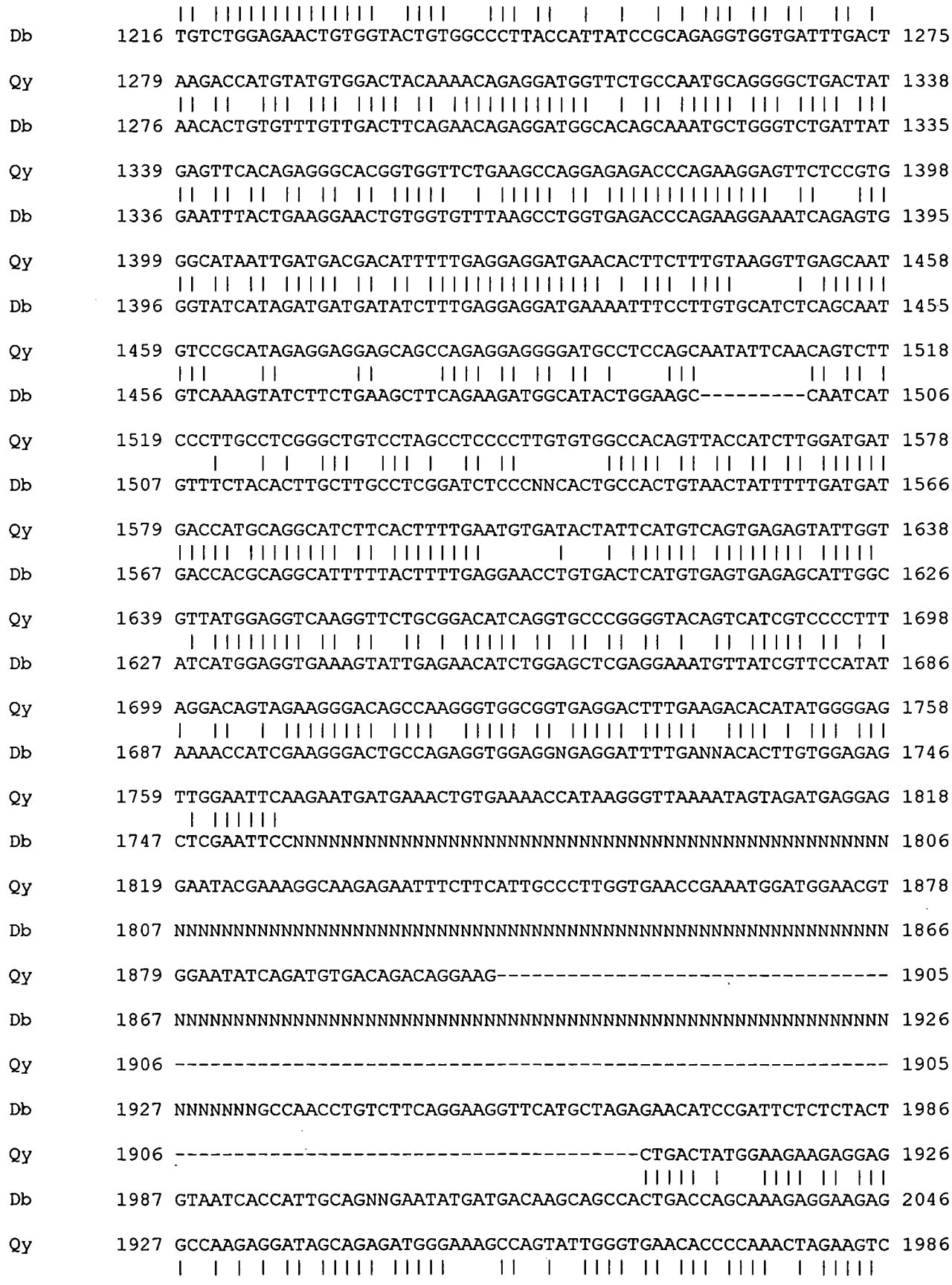

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Db       2047 GAGAGGCGCATTGCAGAAATGGGGCGCCCCATCCTGGGAGAGCACACCAAGTTGGAAGTG 2106

Qy       1987 ATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAAC 2046
              |||||||||||| |||||||| ||||||| ||| |||||||||| || ||||||||||||
Db       2107 ATCATTGAAGAATCCTATGAATTCAAGAGTACTGTGGACAAACTCATTAAGAAGACAAAC 2166

Qy       2047 CTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATCACCGTC 2106
              |||||| | || || |||||  |   |||||| || |||||||| || || ||||| |||
Db       2167 CTGGCCCTTGTGGTTGGGACTAACAGCTGGAGAGAACAGTTCATTGAAGCTATCACTGTC 2226

Qy       2107 AGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTT 2166
              ||||| |  |  ||||| || || ||||||| ||||| |||| |||||||||||| ||
Db       2227 AGTGCTGGGGAAGATGATGACGACGATGAATGTGGGGAAGAGAAGCTGCCCTCCTGTTTC 2286

Qy       2167 GACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCC 2226
              || ||||| |||||||| |||||||| |||||||||| |||||||| || |||||
Db       2287 GATTACGTGATGCACTTTCTGACTGTGTTCTGGAAGGTCTTGTTTGCCTTCGTCCCCCCT 2346

Qy       2227 ACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTC 2286
              || || |||||  | |||||||| || |||  |||||||||||||| |||||| | ||
Db       2347 ACTGAATACTGGAATGGCTGGGCGTGTTTCATTGTCTCCATCCTCATGATTGGCCTACTG 2406

Qy       2287 ACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCA 2346
              || ||  ||||||| |||||||| || ||||| |||||||||||||| || ||||||||
Db       2407 ACAGCTTTCATTGGAGACCTGGCTTCCCACTTTGGCTGCACCATTGGCCTGAAAGATTCT 2466

Qy       2347 GTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAA 2406
              || || || || || ||||| ||| |||| || || || ||||| || ||||||||||||
Db       2467 GTGACTGCAGTCGTGTTCGTCGCACTTGGAACATCAGTGCCAGACACATTTGCCAGCAAA 2526

Qy       2407 GCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAAC 2466
              |  || |||  ||||||    |||||||||||||||| || ||||| ||||||||||||
Db       2527 GTGGCAGCCACCCAGGACCAGTATGCAGACGCCTCCATAGGTAACGTCACGGGCAGCAAC 2586

Qy       2467 GCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCT 2526
              || || || |||||||||| |||||  |||||||||| | || |||||||||   ||
Db       2587 GCGGTGAACGTCTTCCTGGGAATCGGTGTGGCCTGGTCCATCGCTGCCATCTACCACGCA 2646

Qy       2527 CTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTC 2586
                  | ||  |  ||||| | |||||  | |||||||| || ||||| ||||| ||||||
Db       2647 GCCAACGGGGAACAGTTCAAAGTGTCCCCTGGCACACTAGCTTTCTCTGTCACTCTCTTC 2706

Qy       2587 ACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGA 2646
              ||||| ||||| ||  ||    |  | |||||  |||| ||  ||   ||  |     |
Db       2707 ACCATTTTTGCTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGANNCCAGAAANNNGN 2766

Qy       2647 GGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTG 2706
              ||       ||| | |||||      |||||||  ||||   || |||||||||  |||
Db       2767 GGTNNNNNGGGTNGGCCCCGGACTGCCAAGCTCCTCACATNCTGCCTCTTTGTGCTCCTA 2826

Qy       2707 TGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGT 2761
              |||||| | |||||  ||||  || |  | |||||||| ||| |||| || || |
Db       2827 TGGCTCTTGTACATTTTCTTCTCCTCCNTGGAGGCCTACTGCCACATAAAAGGCT 2881


RESULT 11
CNSLT1IBJ
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LOCUS       CNSLT1IBJ               1589 bp    mRNA    linear   HTC 18-JUN-2003
DEFINITION  human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of
            Neuroblastoma of Homo sapiens (human).
ACCESSION   BX248763
VERSION     BX248763.1  GI:28375580
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1589)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1589)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1589
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YD18"
                     /tissue_type="Neuroblastoma"
                     /note="end : 5-PRIME~Cot 10-normalized~vector pCMVSPORT_6"
     CDS             619. .>1589
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                     NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASI
                     EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF
                     IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLY
                     MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE
                     TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDL"
ORIGIN

  Query Match             35.1%;  Score 971;  DB 11;  Length 1589;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-227;
  Matches  971;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 678
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Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       679 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 738

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       739 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 798

Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       799 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 858

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       859 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 918

Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       919 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 978

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       979 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1038

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db      1039 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1098

Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db      1099 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1158

Qy       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1159 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1218

Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db      1219 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1278

Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1279 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1338

Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db      1339 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1398

Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db      1399 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1458

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1459 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1518

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1519 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1578

Qy        961 AAGGATCTGAA 971
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Db       1579 AAGGATCTGAA 1589
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RESULT 12
AK048160

LOCUS	AK048160 3573 bp mRNA linear HTC 20-SEP-2003
DEFINITION	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130038C08 product:solute carrier family 8 (sodium/calcium exchanger), member 1, full insert sequence.
ACCESSION	AK048160
VERSION	AK048160.1 GI:26339181
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3573)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers
source 1. .3573
/organism="Mus musculus"
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/strain="C57BL/6J"
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TEDGTANAGSDYEFTEGTVIFKPGETQKEIRVGIIDDDIFEEDENFLVHLSNVRVSSD
VSEDGILESNHASSIACLGSSSTATITIFDDDHAGIFTFEEPVTHVSESIGIMEVKVL
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KTFFIEIGEPRLVEMSEKKGGFTLTEEYDDKQPLTSKEEEERRIAEMGRPILGEHTKL
EVIIEESYEFKSTVDKLIKKTNLALVVGTNSWREQFIEAITVSAGEDDDDDECGEEKL
PSCFDYVMHFLTVFWKVLFAFVPPTEYWNGWACFIVSILMIGLLTAFIGDLASHFGCT
IGLKDSVTAVVFVALGTSVPGPTL"

ORIGIN

Query Match 34.3%; Score 948.4; DB 11; Length 3573;
Best Local Similarity 67.8%; Pred. No. 9.6e-222;
Matches 1434; Conservative 0; Mismatches 616; Indels 66; Gaps 5;

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Qy        331 GAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAAT 390
              ||  | || || |||||||| |||||||| |||| ||  || ||  |  |  |||||||
Db          2 GAAATAACGATAAAGAAACCGAATGGAGAGACCACCAAGACGACGGTGAGAATCTGGAAC 61

Qy        391 GAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTC 450
              || ||||| || ||||||||| | |||||||||| || |||||||||||||| |||||
Db         62 GAGACTGTGTCGAACCTGACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTG 121

Qy        451 TCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATT 510
              ||  | ||||| ||||| || |||   ||||  || || || ||||| ||    |||||
Db        122 TCAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCCAGCACCATC 181

Qy        511 GTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCA 570
              || || ||||| ||||| |||||||||||||| || |   ||||||| |||||| ||||
Db        182 GTGGGAAGTGCTGCCTTTAACATGTTCATCATAATCGCACTCTGTGTTTACGTGGTCCCT 241

Qy        571 GACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGT 630
              || ||||||||  | |||||||||||||| || || |||||  | || || || |||||
Db        242 GATGGAGAGACAAGGAAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCAGCCTGGAGC 301

Qy        631 ATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAG 690
              |||||||||||  | ||||||  |||||  ||  ||  | |||  |||  |||||  ||  ||  ||
Db        302 ATCTTTGCCTATACCTGGCTTTATATAATCTTGTCTGTCAGCTCTCCTGGAGTTGTGGAG 361

Qy        691 GTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTG 750
              || |||||||||  | ||  |||  ||||||||||||  |  || ||  |  |  || |||||
Db        362 GTCTGGGAAGGCTTGCTTACTTTCTTCTTCTTTCCCATCTGCGTTGTGTTCGCGTGGGTA 421

Qy        751 GCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACAC 810
              |||||  |  ||  ||  |||||  |||||  ||  |  ||||  ||||  |  |  |  |||  ||
Db        422 GCAGACAGGCGGCTTCTCTTTTACAAGTATGTCTACAAGCGGTACAGGGCCGGCAAGCAG 481

Qy        811 CGAGGAATTATCATAGAGACAGAGGGTGACCACCC---------TAAGGGCATTGAGATG 861
               |  ||  ||  |||||  ||     ||  ||  |||    ||           |  |  ||  ||  |||
Db        482 AGGGGGATGATCATTGAACATGAAGGAGACAGACCAGCTTCCAAAACTGAAATCGAAATG 541

Qy        862 GATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGG-------- 913
              |||||||||  ||  |  ||  ||  |||  ||     ||          |  |  |  ||||
Db        542 GATGGGAAAGTGGTCAACTCTCATGTTGACAATTTCTTAGATGGGGCTCTGGTTTTGGAA 601

Qy        914 ----------AAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAG 963
                         |   |  ||  |  ||  ||  ||  |  |  ||||||    |||||||  |||
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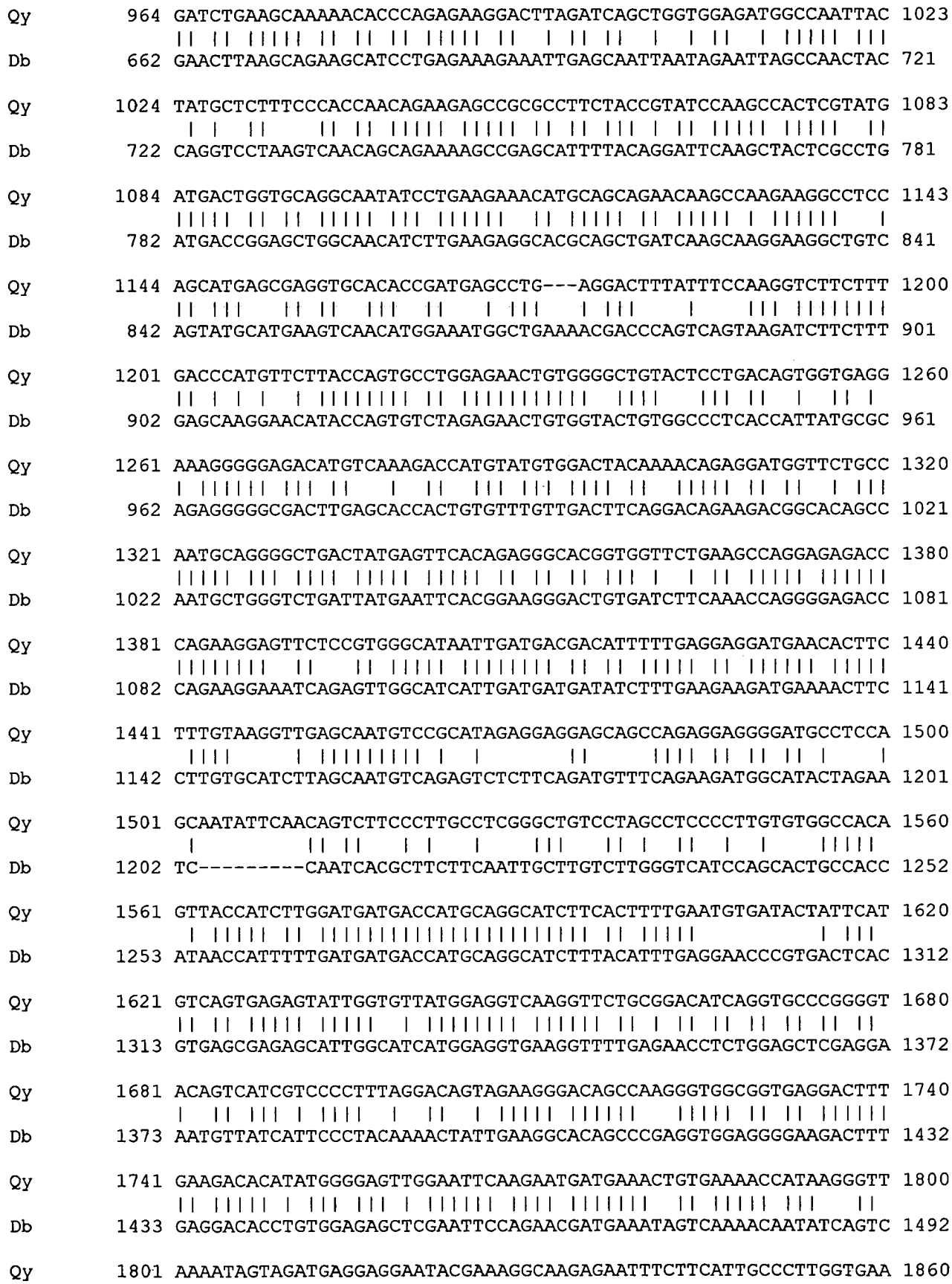

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Db        1493 AAGGTAATCGATGACGAGGAGTATGAGAAAAACAAGACCTTCTTCATTGAGATTGGAGAG 1552

Qy        1861 CCGAAATGGATGGA--------------------------ACGTGGAATATCAGATGTG 1893
                ||       | ||||                       |      |      | |||
Db        1553 CCCCGTCTGGTGGAGATGAGTGAGAAGAAAGGTGGCTTCACATTAACAGAGGAATATGAT 1612

Qy        1894 ACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAG 1953
                   |   |   |||||  |   ||||||||||||   | |  |  ||  ||  ||  |||||
Db        1613 GACAAGCAGCCACTGACCAGCAAAGAAGAGGAGGAGAGGCGCATTGCGGAAATGGGGCGC 1672

Qy        1954 CCAGTATTGGGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAG 2013
                ||   |   |  ||  ||  |||  ||||  ||  ||  ||  |||||  ||||||||  ||  ||  ||||||
Db        1673 CCCATCCTAGGCGAGCACACCAAGCTGGAGGTGATCATCGAAGAGTCTTACGAATTCAAG 1732

Qy        2014 ACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCC 2073
                |  ||  ||||||||||||  ||  ||||||||  |||||||||  |  ||  |||||||||  |    |
Db        1733 AGCACTGTGGACAAACTCATTAAGAAGACGAACCTGGCCCTTGTGGTGGGGACCAACAGC 1792

Qy        2074 TGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGAT 2133
                |||||  ||  |||||  ||  ||  ||||||||  |||||  ||  |   |   |||||  |||||  |||
Db        1793 TGGAGAGAGCAGTTTATCGAAGCCATCACTGTCAGCGCTGGGGAAGATGACGATGATGAT 1852

Qy        2134 GAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTC 2193
                ||||  ||||||||||  ||||||||||||  |||||  |||||  ||||||||  ||  ||  ||
Db        1853 GAATGTGGGGAGGAGAAGCTGCCCTCCTGTTTTGATTACGTGATGCACTTTCTCACAGTG 1912

Qy        2194 TTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGC 2253
                ||||||||||||  ||||||||||  ||  ||  ||  |||||  |||||  |  ||||||||||||
Db        1913 TTCTGGAAGGTTCTGTTTGCCTTCGTCCCACCTACAGAATACTGGAATGGCTGGGCCTGC 1972

Qy        2254 TTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCG 2313
                |||   ||||||||||||||  ||  |||  |  ||  ||||||  |||||||  ||||||||  ||
Db        1973 TTCATTGTCTCCATCCTCATGATCGGCCTACTGACCGCCTTCATTGGAGACCTGGCTTCC 2032

Qy        2314 CACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTT 2373
                |||||  ||||||||||||||||||  ||||||||  ||  ||  ||  |||||  ||  ||  ||  ||
Db        2033 CACTTTGGCTGCACCATTGGTCTGAAAGATTCCGTGACTGCCGTTGTGTTTGTTGCTCTT 2092

Qy        2374 GGCACCTCTGTCCCAG 2389
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Db        2093 GGAACCTCGGTGCCAG 2108
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RESULT 13
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LOCUS       BX374548                941 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX374548 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
            cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.
ACCESSION   BX374548
VERSION     BX374548.1  GI:30438490
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
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  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7256.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DB006DB09_DB1287_2&cluster=7256.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DB006DB09_DB1287_2.
FEATURES             Location/Qualifiers
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                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
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                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             32.5%;  Score 899.6;  DB 13;  Length 941;
  Best Local Similarity   97.7%;  Pred. No. 4.6e-210;
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Qy        685 GTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCC 744
              | |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          1 GGCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCC-GTGTGTGTCCTTCTGGCC 59

Qy        745 TGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGAC 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGAC 119

Qy        805 AAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGAT 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 AAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGAT 179

Qy        865 GGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAA 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAA 239

Qy        925 GTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCA 984
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Db        240 GTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCA 299

Qy        985 GAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAG 1044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1045 AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC 1104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC 419

Qy       1105 CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC 1164
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Db        420 CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC 479

Qy       1165 GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG 1224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG 539

Qy       1225 GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACC 1284
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Db        540 GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACC 599

Qy       1285 ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC 1344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC 659

Qy       1345 ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA 1404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA 719

Qy       1405 ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGC 1464
             |||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        720 ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGNTAGGTTGAGCAATGTCCGC 779

Qy       1465 ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTG 1524
             |||||||||||||||||||||||||||||||      ||||||||      | |||||
Db        780 ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTNNCAGCATATTCAAACAGTCTTCCTTG 839

Qy       1525 CCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCAT 1584
             |||||||||||||||||| |||||| |||| ||||||||||||||||||||||||||||
Db        840 CCTCGGGCTGTCCTAGCCTNCCCTTGNGTGGNCACAGTTACCATCTTGGATGATGACCAT 899

Qy       1585 GCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 1625
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DEFINITION  Mus musculus HCM3309 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY408695
VERSION     AY408695.1  GI:39764666
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2515)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2515)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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  Matches 1348;  Conservative    0;  Mismatches  708;  Indels   52;  Gaps    6;

Qy        691 GTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTG 750
              || ||||| |  || ||||| ||  ||||||| || |||||||| |  | |||||| ||
Db        426 GTGTGGGAGGCACTGCTCACACTGATCTTCTTCCCGGTGTGTGTGGTGTTTGCCTGGATG 485

Qy        751 GCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACAC 810
              || || || |||||||||||||||||| ||| || ||||    |||||||| |||   | |
Db        486 GCGGACAAGCGACTGCTCTTCTACAAGTACGTGTACAAGCGCTACCGCACCGACCCTCGC 545

Qy        811 CGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGGGAAA 870
               | ||||| ||||| | | ||||||| ||||  || ||| |||| ||| |||| || | |
Db        546 AGTGGAATCATCATCGGGGCAGAGGGAGACCCACCCAAGAGCATCGAGCTGGACGGCACA 605

Qy        871 ATGATGAATTCCCATTTTCTAGATG----------GGAACCTGGTGCCCCTGGAAGGG 918
               |  ||    |  |  | |  |  |             |  |   |  ||    || | |
Db        606 TTCGTGGGCACTGAGGTCCCTGGCGAGCTGGGCGCATTGGGCACAGGTCCTGCTGAGGCG 665

Qy        919 AAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA 978
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Db        666 CGTGAACTAGATGCCAGCCGGCGTGAGGTCATCCAGATCCTTAAGGACTTGAAGCAGAAG 725

Qy        979 CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAC 1038
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Db        726 CACCCGGATAAGGACCTGGAGCAGCTGATGGGCATCGCCAAGTACTATGCACTGCTGCAC 785

Qy       1039 CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC 1098
              || |||||||||||||||||||||| ||||| ||||| ||  ||||||| ||||| |||
Db        786 CAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACGCGGCTGATGACAGGTGCGGGC 845

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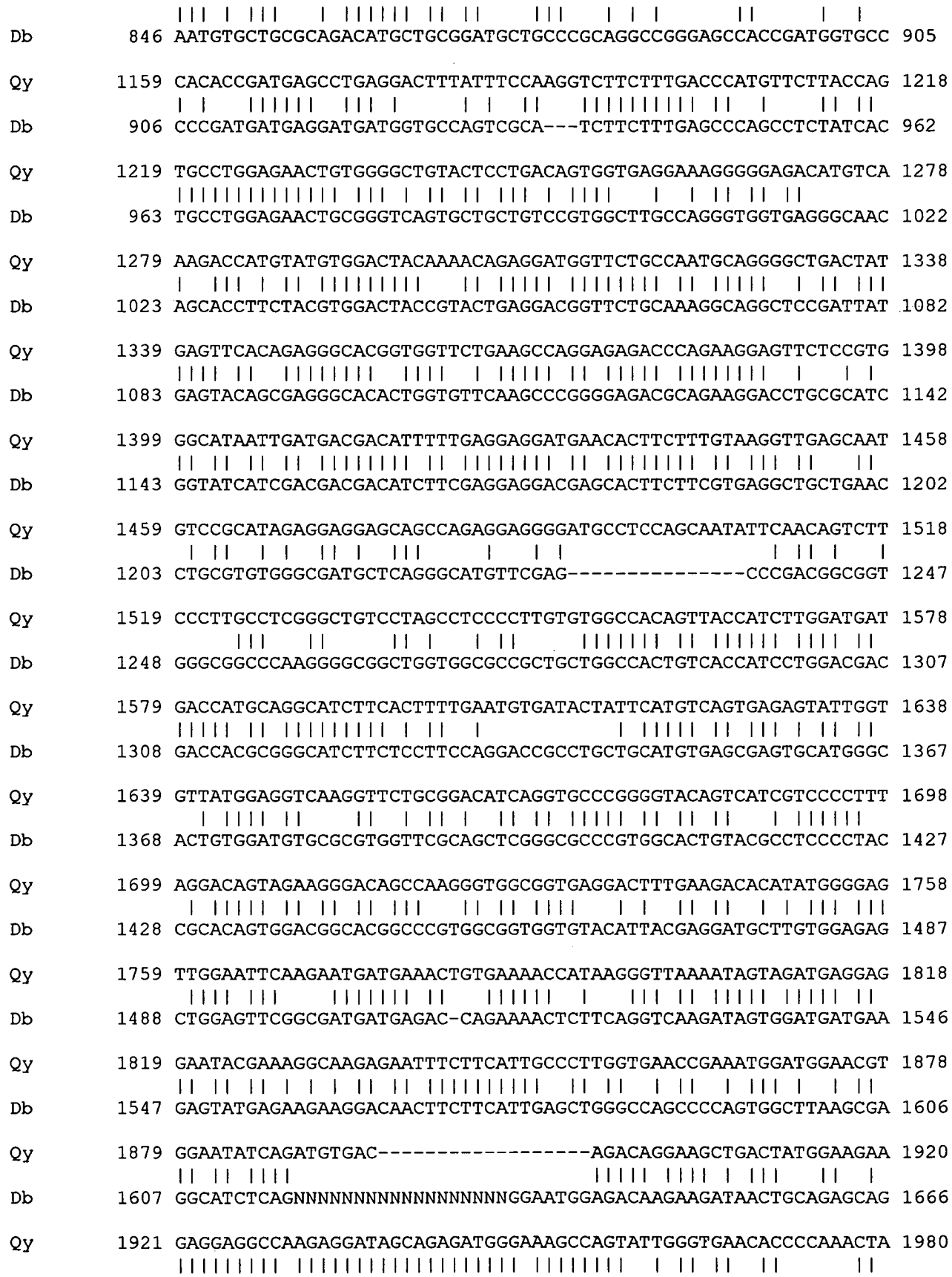

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Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Db       1727 GAGGTCATCATCGAGGAGTCTTATGACTTTAAGNNNNNNNNNNNNNNNNNNNNNNNNNN 1786

Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100

Db       1787 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1846

Qy       2101 ACCGTCAGTGCA---GCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC 2157
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Db       1847 NNNNNNNNNNNNNGGGACGAGGAGGAGGATGAGGATGGACCTCGTGAGGAGCGGCTGCCG 1906

Qy       2158 TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT 2217
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Qy       2218 GTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT 2277
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Db       1967 GTTCCACCCACGGAGTACTGCAATGGCTGGGCCTGCTTTGGTGTCTGCATCCTGGTCATT 2026

Qy       2278 GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC 2337
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Db       2027 GGTGTGCTCACTGCCCTCATCGGAGACCTGGCCTCACACTTTGGGTGCACCGTGGGCCTC 2086

Qy       2338 AAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTT 2397
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Qy       2398 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG 2457
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Qy       2458 GGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC 2517
              |||  |||  ||  ||  ||  ||  |||||||||  |  ||  ||||||||||  |||||  ||  |
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Qy       2518 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTC 2577
              ||||||||  |||||||  |      |||  |  |||    ||  |||||  ||||||||||  |||
Db       2267 TACTGGGCGGTGCAGGGTCGCCCCTTCGAGGTGCGTGCAGGCACGCTGGCCTTCTCGGTC 2326

Qy       2578 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG 2637
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Qy       2638 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2697
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Db       2387 CAGATTGGCGGCGAGCTGGGCGGCCCGCGGGGACCCAAGCTGGCCACCACCGCTCTCTTC 2446

Qy       2698 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2757
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Db       2447 CTGGGCCTCTGGTTCCTCTACATTCTCTTCTCCAGCCTGGAGGCTTACTGCCACATCCGG 2506

Qy       2758 GGGTTCTA 2765
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Db       2507 GGCTTCTA 2514
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RESULT 15
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DEFINITION 603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5', mRNA sequence.
ACCESSION BI913344
VERSION BI913344.1 GI:16177710
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11613 row: m column: 05
High quality sequence stop: 782.
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/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
ORIGIN

Query Match 29.4%; Score 813.8; DB 12; Length 887;
Best Local Similarity 97.2%; Pred. No. 6.1e-189;
Matches 860; Conservative 0; Mismatches 22; Indels 3; Gaps 3;

Qy 916 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 975
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Db 1 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 60

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Qy        976 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 1035
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Qy       1036 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 1095
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Qy       1096 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 1155
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Qy       1156 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 1215
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Db        241 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 300

Qy       1216 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 1275
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Qy       1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
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Qy       1336 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395
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Qy       1396 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 1455
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Db        541 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 600

Qy       1516 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
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Search completed: June 25, 2004, 15:31:14
Job time : 6359.47 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 04:06:20 ; Search time 10407.3 Seconds
(without alignments)
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Title: US-10-054-680-1
Perfect score: 2766
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	2766	100.0	3812	6	AX496815	AX496815 Sequence
	3	2764.4	99.9	2966	6	AX480881	AX480881 Sequence
	4	2764.4	99.9	5250	9	AF510501	AF510501 Homo sapi
	5	2761.2	99.8	2782	6	AX476818	AX476818 Sequence
	6	2737.4	99.0	2837	9	HSA304853	AJ304853 Homo sapi
	7	2736.4	98.9	5268	9	AF510502	AF510502 Homo sapi
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	10	2546.4	92.1	5146	9	AF510503	AF510503 Homo sapi
	11	2398	86.7	4640	10	BC052435	BC052435 Mus muscu
	12	2352.4	85.0	4854	10	RNU53420	U53420 Rattus norv
	13	2312.8	83.6	3838	9	HSA508602	AJ508602 Homo sapi
	14	2290.2	82.8	3435	10	AF453257	AF453257 Mus muscu
	15	1786.4	64.6	2534	9	HSNCX22	X93017 Homo sapien
	16	1784.8	64.5	126512	6	AX476820	AX476820 Sequence
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	28	1302.6	47.1	2805	10	AF109163	AF109163 Rattus no
	29	1301	47.0	2805	10	AF109166	AF109166 Rattus no
	30	1294.4	46.8	3037	10	RNSCEA1	X68812 R.norvegicu
	31	1277	46.2	4282	9	AB029010	AB029010 Homo sapi
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38	1232	44.5	2874	10	AF109164	AF109164 Rattus no
39	1230.4	44.5	3303	10	RNU04933	U04933 Rattus norv
40	1227.8	44.4	4087	4	BOVEXCHANG	L06438 Bos taurus
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ALIGNMENTS

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DEFINITION  Sequence 1 from Patent WO02059316.
ACCESSION   AX496811
VERSION     AX496811.1  GI:23342335
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE     Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 1 01-AUG-2002;
            LEXICON GENETICS INC (US)
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ORIGIN

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  Matches 2766;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
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Db       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
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Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Db       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640

Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Db       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Qy       2761 TTCTAA 2766
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Db       2761 TTCTAA 2766


RESULT 2
AX496815
LOCUS       AX496815               3812 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from Patent WO02059316.
ACCESSION   AX496815
VERSION     AX496815.1  GI:23342337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE     Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 5 01-AUG-2002;
            LEXICON GENETICS INC (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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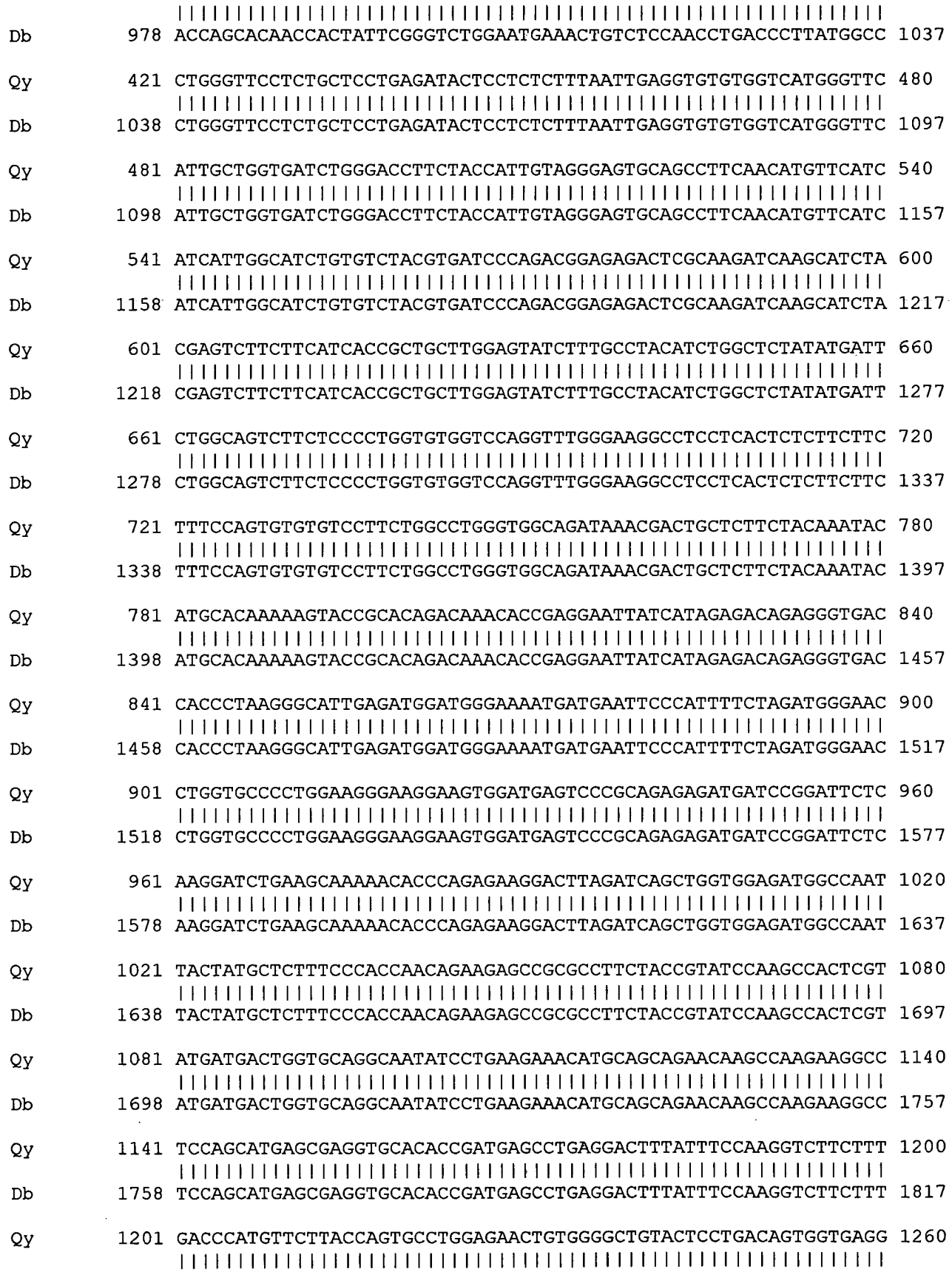

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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1938 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db       1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 2417

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
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Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
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Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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Db       3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy       2761 TTCTAA 2766
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RESULT 3
AX480881
LOCUS       AX480881               2966 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 41 from Patent WO0246415.
ACCESSION   AX480881
VERSION     AX480881.1  GI:22217538
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lee,E.A., Baughn,M.R., Yue,H., Ding,L., Raumann,B.E., Hafalia,A.J.,
            Khan,F.A., Nguyen,D.B., Elliott,V.S., Ramkumar,J., Walia,N.K.,
            Ison,C.H., Lu,Y., Gandhi,A.R., Warren,B.A., Duggan,B.M.,
            Tribouley,C.M., Burford,N., Lu,D.A., Lal,P.G., Yao,M.G., Xu,Y.,
            Bruns,C.M., Thangavelu,K., Swarnakar,A., Tang,Y.T., Azimzai,Y.,
            Thornton,M., Arvizu,C. and Policky,J.L.
  TITLE     Transporters and ion channels
  JOURNAL   Patent: WO 0246415-A 41 13-JUN-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 2765;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        321 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 380

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        381 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 440

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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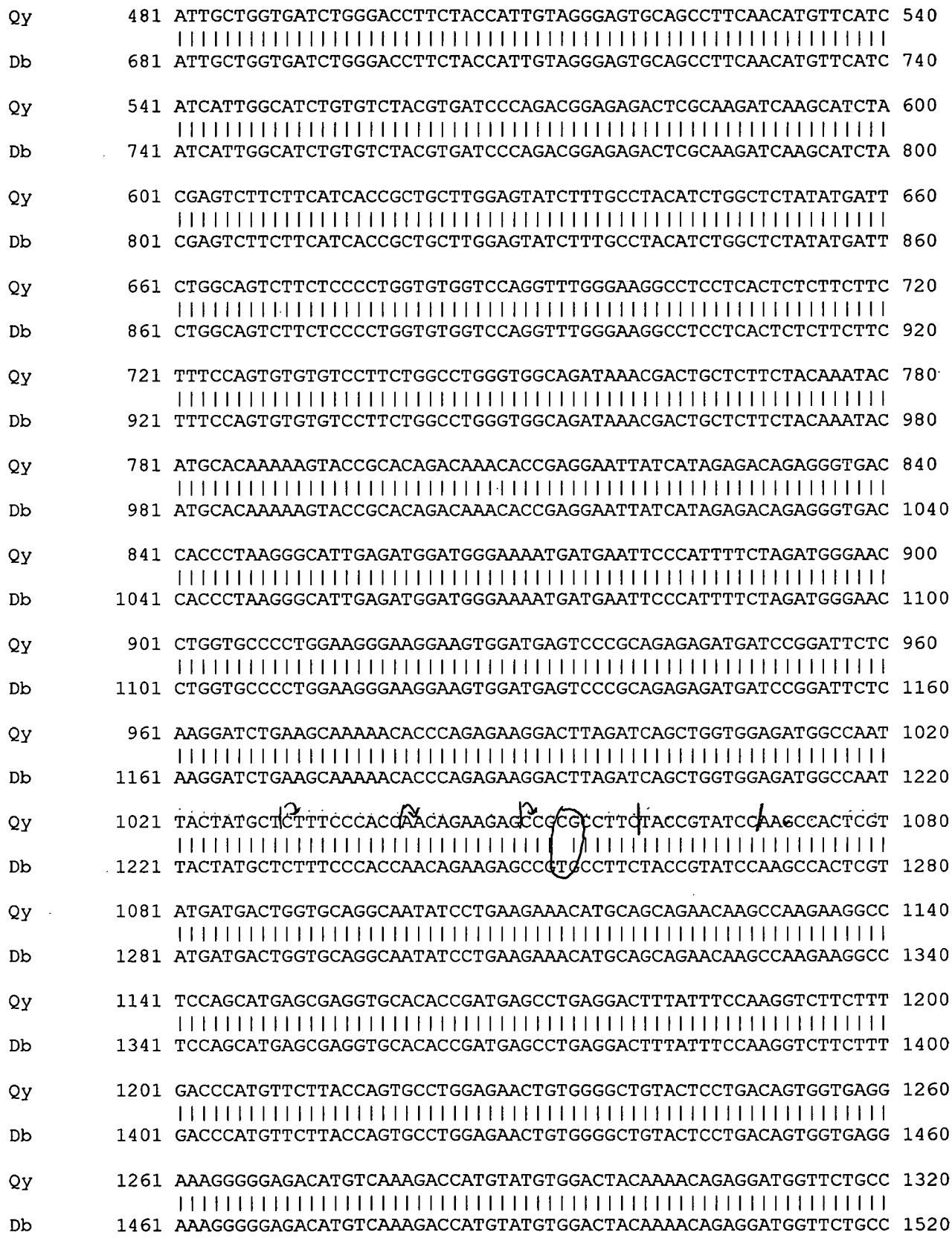

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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Db       2601 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2660

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Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Qy       2761 TTCTAA 2766
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Db       2961 TTCTAA 2966


RESULT 4
AF510501
LOCUS       AF510501               5250 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 2 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510501
VERSION     AF510501.1  GI:24421220
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5250)
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  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5250)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
            G. Colombo, Padova, PD 35131, Italy
FEATURES             Location/Qualifiers
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     CDS             755. .3520
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ORIGIN

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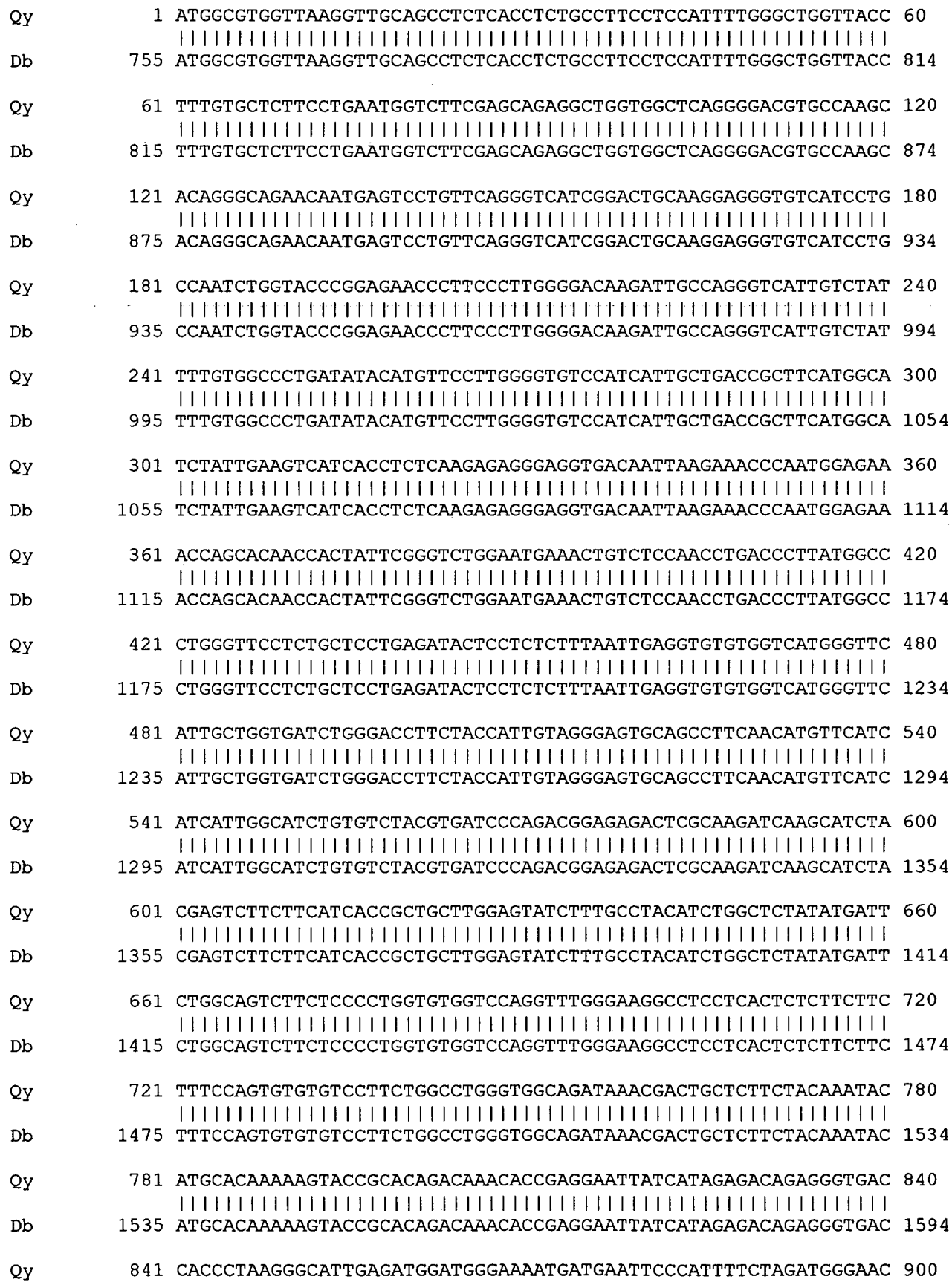

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Db       1655 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1714

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                                                                                
Db       1715 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1774

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                                                                                
Db       1775 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1834

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                                                                                
Db       1835 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1894

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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
                                                                                
Db       1955 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 2014

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                                                                                
Db       2015 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 2074

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                                                                                
Db       2075 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 2134

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Db       2135 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2194

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
                                                                                
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                                                                                
Db       2255 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2314

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
                                                                                
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                                                                                
Db       2375 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2434

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                                                                                
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Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
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Db       2675 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 2734

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Db       2735 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2794

Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
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Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
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Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
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Db       3455 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3514

Qy       2761 TTCTAA 2766
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Db       3515 TTCTAA 3520


RESULT 5
AX476818
LOCUS       AX476818               2782 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1 from Patent WO0233086.
ACCESSION   AX476818
VERSION     AX476818.1  GI:22216098
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
            Beasley,E.M.
  TITLE     Isolated human transporter proteins, nucleic acid molecules
            encoding human transporter proteins, and uses thereof
  JOURNAL   Patent: WO 0233086-A 1 25-APR-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
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ORIGIN

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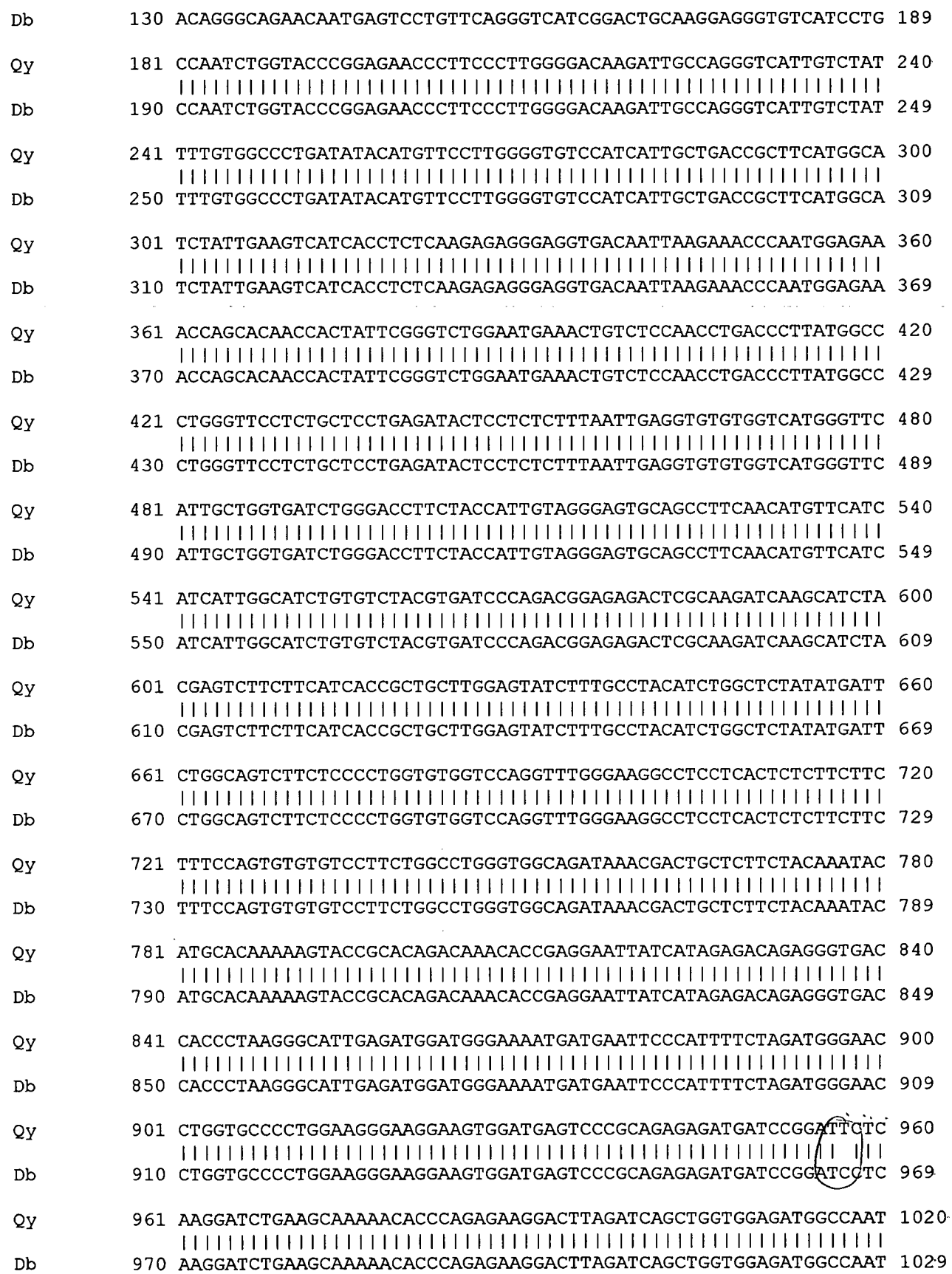
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Db       1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089

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Db       1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209

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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
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Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Qy        2761 TTCTAA 2766
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Db        2770 TTCTAA 2775


RESULT 6
HSA304853
LOCUS       HSA304853               2837 bp    mRNA    linear   PRI 06-JUN-2001
DEFINITION  Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative
            splice form B (SCL8A3 gene).
ACCESSION   AJ304853
VERSION     AJ304853.1  GI:14330384
KEYWORDS    alternative splicing; form B; SCL8A3 gene; SCL8A3 protein;
            Sodium/calcium exchanger.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gabellini,N.
  TITLE     Characterization of the human SCL8A3 gene for solute carrier family
            8, member 3 (sodium/calcium exchanger)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2837)
  AUTHORS   Bortoluzzi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and
            Department of Biological Chemistry, University of Padova, via G.
            Colombo 3, 35131 PADOVA, ITALY
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 99.0%; Score 2737.4; DB 9; Length 2837;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2760; Conservative 0; Mismatches 6; Indels 9; Gaps 1;

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Db         63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 122

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Db        2523 GTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCC 2582

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RESULT 7
AF510502
LOCUS       AF510502                5268 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 3 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510502
VERSION     AF510502.1  GI:24421222
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5268)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5268)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
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  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
            G. Colombo, Padova, PD 35131, Italy
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                     MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE
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  Matches 2765;  Conservative    0;  Mismatches    1;  Indels   18;  Gaps    1;

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Db        755 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 814

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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RESULT 8
AX299471
LOCUS       AX299471               2781 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 1 from Patent WO0183744.
ACCESSION   AX299471
VERSION     AX299471.1  GI:17129228
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wilm,C.
  TITLE     Natrium-calcium exchanger protein
  JOURNAL   Patent: WO 0183744-A 1 08-NOV-2001;
            MERCK PATENT GmbH (DE)
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ORIGIN

  Query Match             98.8%;  Score 2733.4;  DB 6;  Length 2781;
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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DEFINITION  Homo sapiens mRNA for sodium/calcium exchanger SCL8A3, alternative
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ACCESSION   AJ304852
VERSION     AJ304852.1  GI:14330382
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Gabellini,N.
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2840)
  AUTHORS   Bortoluzzi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and
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            Colombo 3, 35131 PADOVA, ITALY
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ORIGIN

Query Match 96.1%; Score 2657.6; DB 9; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

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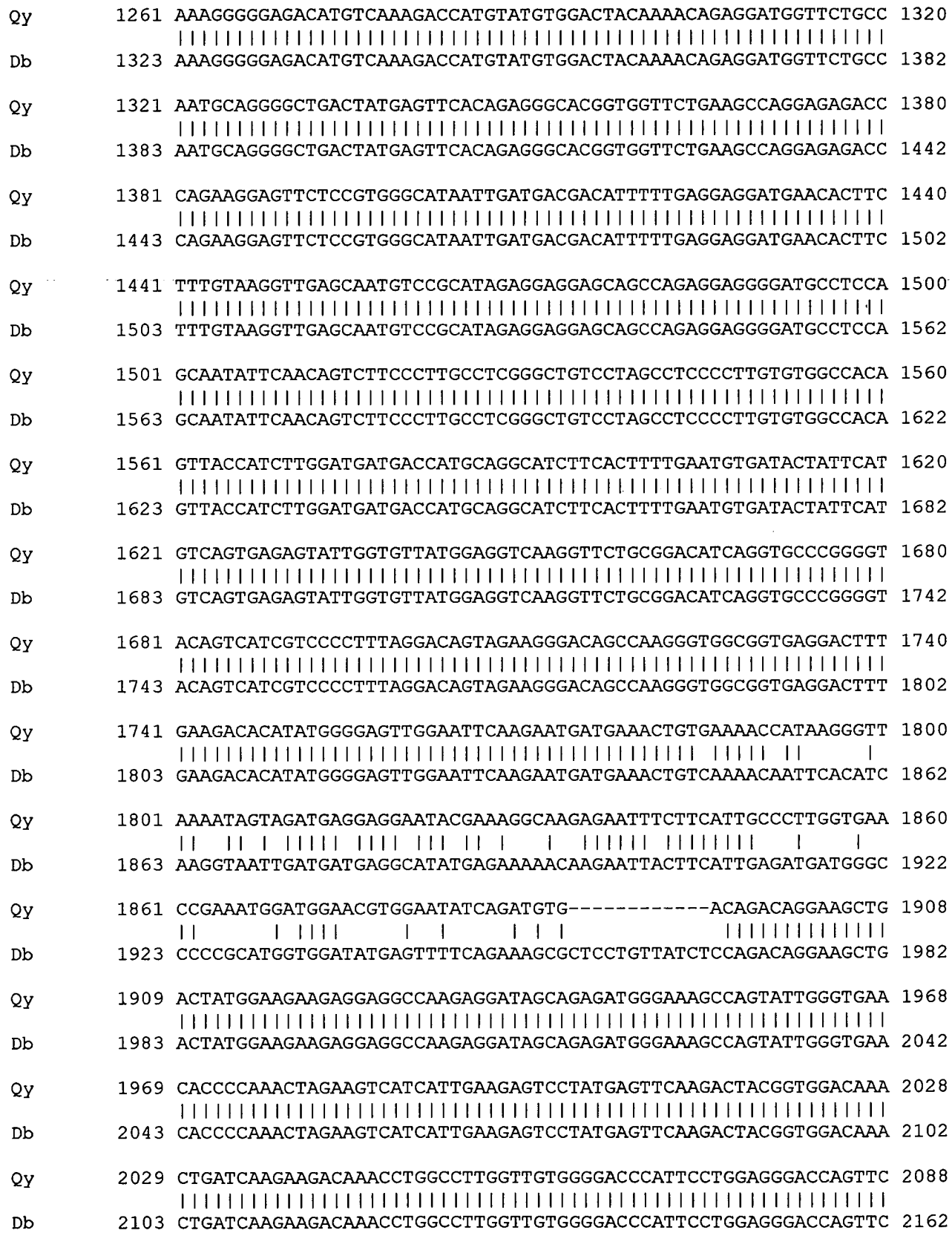

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Qy       2449 AACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTG 2508
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RESULT 10
AF510503
LOCUS       AF510503               5146 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 4 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510503
VERSION     AF510503.1  GI:24421224
KEYWORDS    .
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SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 5146)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5146)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
            G. Colombo, Padova, PD 35131, Italy
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ORIGIN

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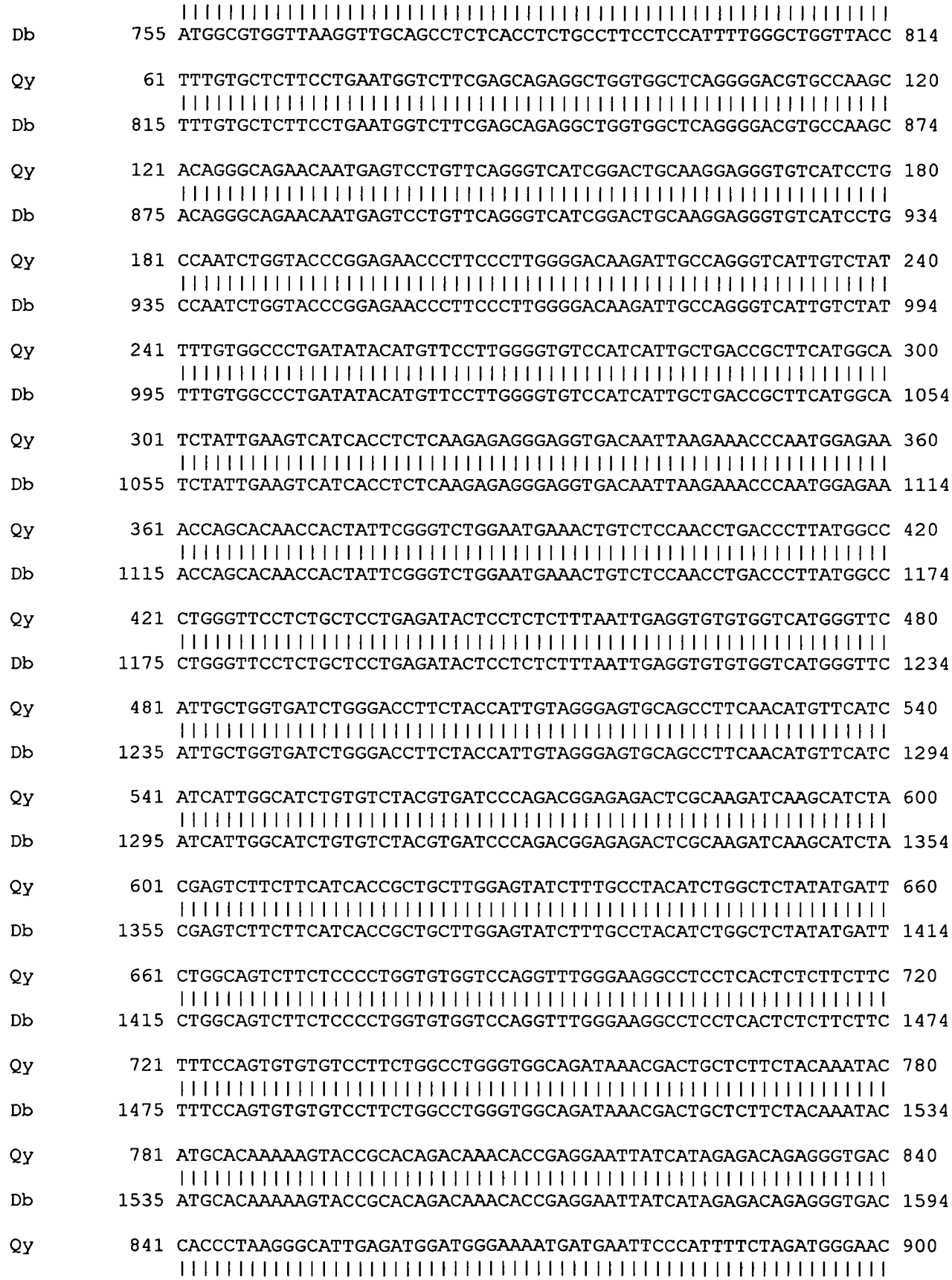

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RESULT 11
BC052435
LOCUS BC052435 4640 bp mRNA linear ROD 07-OCT-2003
DEFINITION Mus musculus solute carrier family 8 (sodium/calcium exchanger), member 3, mRNA (cDNA clone MGC:63358 IMAGE:6837128), complete cds.
ACCESSION BC052435
VERSION BC052435.1 GI:30851384
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4640)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 4640)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (15-MAY-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0.

FEATURES Location/Qualifiers

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ORIGIN

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Db        613 TTTGTGGCCCTGATATACATGTTTCTTGGGGTGTCTATCATTGCTGACCGATTCATGGCA 672

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              |||||||||||||| || || |||||||||| ||||| || ||||| ||||||||||
Db        673 TCTATTGAAGTCATTACTTCCCAAGAGAGGGAAGTGACCATCAAGAAGCCCAATGGAGAG 732

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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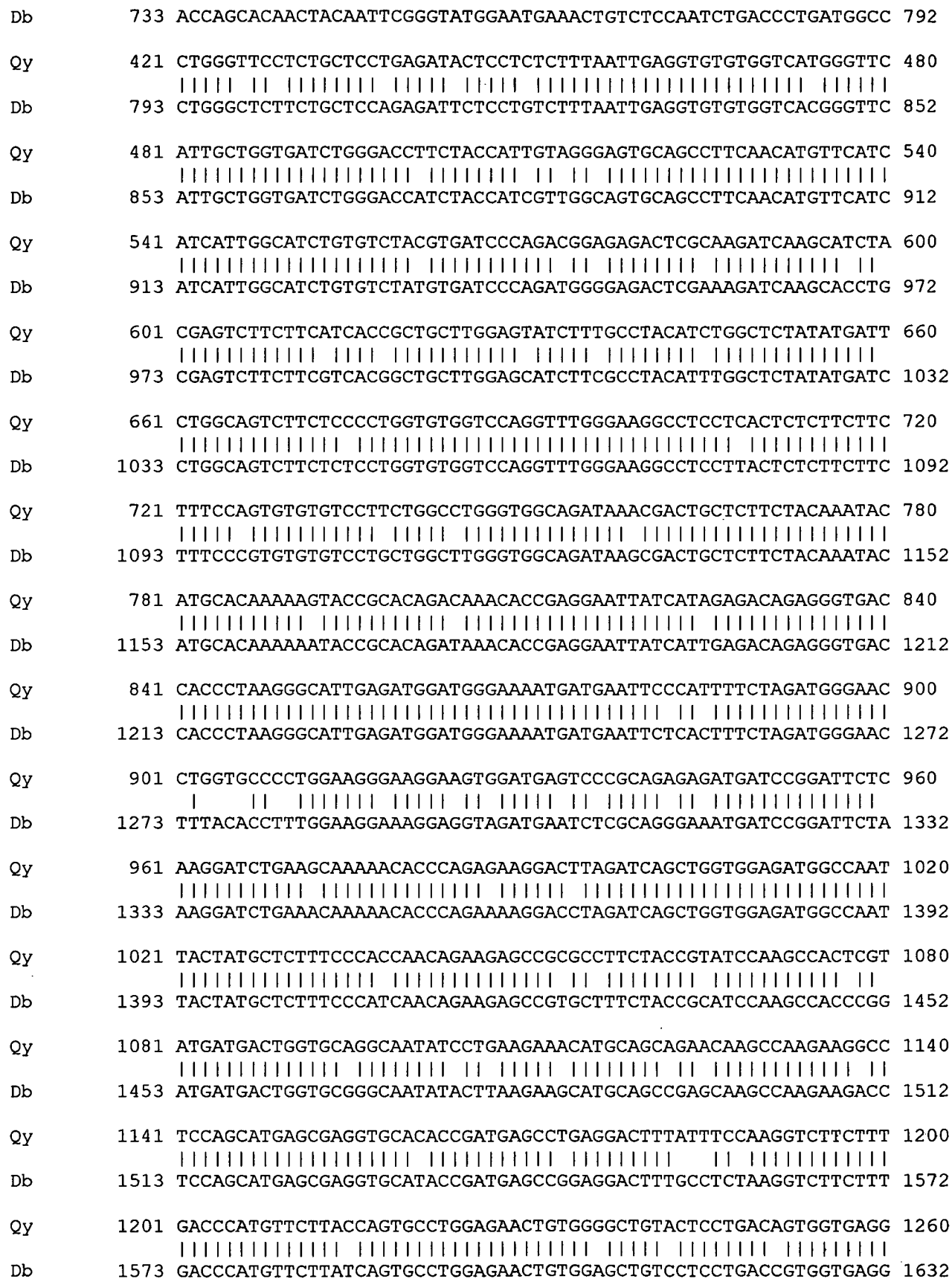

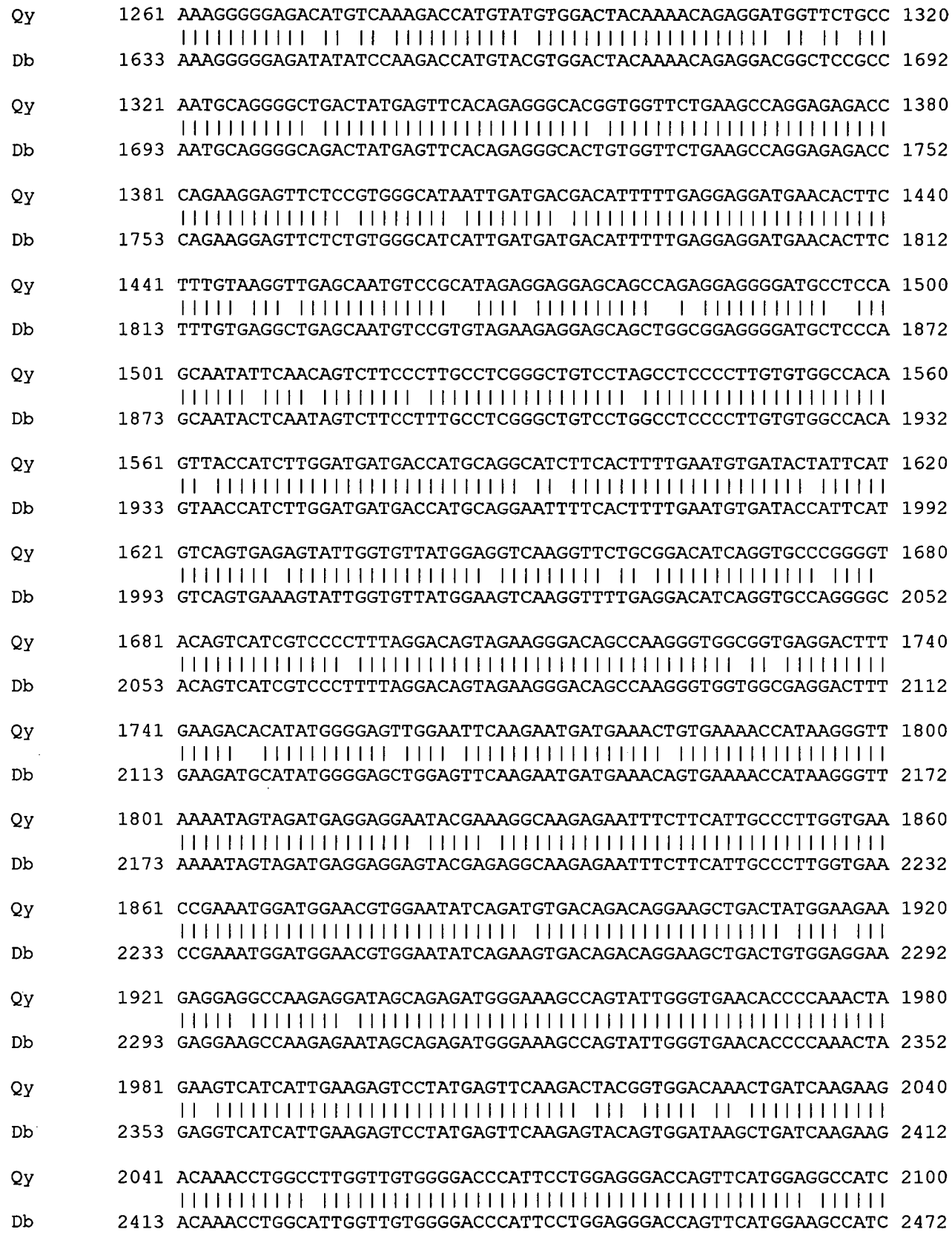

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Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Db       2473 ACTGTTAGTGCAGGAGGGGATGAGGATGAAGACGAATCTGGAGAGGAGAGGCTGCCATCC 2532

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
              |||||||||||||||||||||||||||| ||||||||||||||| ||||||||||||
Db       2533 TGCTTTGACTACGTCATGCACTTCCTGACGGTCTTCTGGAAGGTGCTCTTTGCCTGTGTG 2592

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Db       2593 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGTGGTCTCCATCCTCATTATTGGC 2652

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
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Db       2653 ATGCTCACCGCCATCATCGGGGACCTGGCCTCTCACTTCGGCTGCACCATCGGGCTCAAG 2712

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
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Db       2713 GATTCGGTCACAGCTGTTGTTTTTGTGGCATTCGGCACCTCTGTGCCAGATACATTTGCC 2772

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Db       2773 AGCAAAGCCGCTGCCCTGCAGGACGTGTATGCAGATGCTTCCATTGGCAACGTCACAGGC 2832

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Db       2953 CTTTTCACCATCTTTGCATTTGTCTGCCTCAGTGTGCTCTTGTATCGTCGGCGGCCCCAT 3012

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Db       3013 CTGGGCGGGGAGCTCGGAGGTCCTCGTGGCTGCAAGCTTGCCACGACATGGCTCTTTGTG 3072

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Db       3073 AGCCTATGGCTCCTCTACATACTATTTGCCACGCTGGAGGCCTACTGCTACATCAAGGGG 3132

Qy       2761 TTCTAA 2766
              |||| |
Db       3133 TTCTGA 3138
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RESULT 12
RNU53420
LOCUS       RNU53420                4854 bp    mRNA    linear   ROD 04-OCT-1996
DEFINITION  Rattus norvegicus sodium-calcium exchanger form 3 (NCX3) mRNA,
            complete cds.
ACCESSION   U53420
VERSION     U53420.1  GI:1552525
KEYWORDS    .
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```
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 4854)
  AUTHORS   Nicoll,D.A., Quednau,B.D., Qui,Z., Xia,Y.R., Lusis,A.J. and
            Philipson,K.D.
  TITLE     Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3
  JOURNAL   J. Biol. Chem. 271 (40), 24914-24921 (1996)
  MEDLINE   96394663
   PUBMED   8798769
REFERENCE   2  (bases 1 to 4854)
  AUTHORS   Nicoll,D.A. and Philipson,K.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1996) Physiology, University of California, Los
            Angeles, 3645 MRLB, 675 Circle Dr. S., Los Angeles, CA 90095-1760,
            USA
FEATURES             Location/Qualifiers
     source          1. .4854
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                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
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                     /map="tightly linked to D12Ucla3"
                     /note="maps to chromosome 12 in mouse and 14q21-31 in
                     human"
     gene            1. .4854
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     CDS             834. .3617
                     /gene="NCX3"
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                     IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFVTAAWSVFAYIWLY
                     MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIE
                     TEGEHPKGIEMDGKMMNSHFLDGNLIPLEGKEVDESRREMIRILKDLKQKHPEKDLDQ
                     LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKTASMSEVHTDEPE
                     DFASKVFFDPCSYQCLENCGAVLLTVVRKGGDISKTMYVDYKTEDGSANAGADYEFTE
                     GTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRVEEEQLEEGMTPAILNSLPL
                     PRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPF
                     RTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWM
                     ERGISALLLSPEVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKSTVDK
                     LIKKTNLALVVGTHSWRDQFMEAITVSAAGDEEEDESGEERLPSCFDYVMHFLTVFWK
                     VLFACVPPTEYCHGWACFVVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFG
                     TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWAMQGQEFHV
                     SAGTLAFSVTLFTIFAFVCLSVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYVL
                     FATLEAYCYIKGF"
ORIGIN

  Query Match           85.0%;  Score 2352.4;  DB 10;  Length 4854;
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Best Local Similarity 90.7%; Pred. No. 0;
Matches 2525; Conservative 0; Mismatches 241; Indels 18; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||  ||  ||||||||||||||||||||||||||||||  ||||||||||
Db        834 ATGGCGTGGTTACGGCTGCAGCCTCTCACCTCTGCCTTCCTCCATTTCGGGCTGGTTACT 893

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||  ||    ||||  |||||  ||
Db        894 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGACTTGAGGGATGTGCCCAGT 953

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
               ||||  ||||||||||||||||||||||||||||  ||||||||||||||||||||  ||
Db        954 GCAGGACAGAACAATGAGTCCTGTTCAGGGTCATCAGACTGCAAGGAGGGTGTCATCTTG 1013

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||  ||  ||||||||||||||||||||||||||||  ||||||||||||||
Db       1014 CCAATCTGGTATCCAGAGAACCCTTCCCTTGGGGACAAGATTGCAAGGGTCATTGTCTAT 1073

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||  |||||  |||||  ||||||||||||  |||||||||
Db       1074 TTTGTGGCCCTGATATACATGTTTCTTGGAGTGTCTATCATTGCTGACCGATTCATGGCA 1133

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db       1134 TCTATTGAAGTTATTACCTCCCAAGAGAGGGAGGTGACAATCAAGAAGCCCAATGGAGAG 1193

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||  ||  ||||||||  ||||||||||||||||||||||||||||||  ||||||
Db       1194 ACCAGCACAACTACAATTCGGGTATGGAATGAAACTGTCTCCAACCTGACCCTGATGGCC 1253

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||  ||  ||  ||||||||  |||||  |||||  ||||||||||||||||||||||  ||||||
Db       1254 CTAGGCTCTTCTGCTCCGGAGATTCTCCTGTCTTTAATTGAGGTGTGTGGTCACGGGTTC 1313

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||  |||||||  ||||||||||  ||  ||||||||||||||||||||||
Db       1314 ATTGCTGGTGATTTGGGACCGTCTACCATTGTCGGCAGTGCAGCCTTCAACATGTTCATC 1373

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||  ||||||||||  ||  ||||||||||||||||||  ||
Db       1374 ATCATTGGCATCTGTGTCTATGTGATCCCAGATGGGGAGACTCGCAAGATCAAGCACCTT 1433

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||  ||||  ||||||||||  |||||||||  ||  ||||||||  |||||
Db       1434 CGAGTCTTCTTTGTCACGGCTGCTTGGAGCGTCTTTGCCTATATTTGGCTCTACATGATC 1493

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||  ||||||||||||||||||||||||||||||  ||||||||||||
Db       1494 CTGGCAGTCTTCTCTCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTTACTCTCTTCTTC 1553

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1554 TTTCCAGTGTGTGTCCTGCTGGCTTGGGTGGCAGATAAGCGACTGCTCTTCTACAAATAC 1613

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1614 ATGCACAAAAGATACCGCACAGATAAACACCGAGGAATTATCATTGAGACAGAGGGTGAA 1673

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              |||||||||||||||||||||||||||||||||||||||||||| || || || |||||||||
Db       1674 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCTCACTTCCTGGATGGGAAC 1733

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||  | ||| ||||||| ||||| || ||||| || ||||| || |||||||| |||||
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       1794 AAGGATCTGAAGCAAAAACACCCAGAAAAAGACTTAGATCAGCTGGTGGAGATGGCCAAT 1853

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              |||||||||||||||||||||||||||||| || |||||||| |||||||||| ||
Db       1854 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCTTTCTACCGCATCCAAGCCACCCGG 1913

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1914 ATGATGACTGGTGCAGGCAATATACTTAAGAAACATGCAGCAGAGCAAGCCAAGAAGACC 1973

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1974 GCCAGCATGAGTGAGGTGCATACTGATGAGCCTGAGGACTTTGCCTCGAAGGTCTTTTTT 2033

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       2454 GTCAGTGAAAGTATTGGTGTTATGGAAGTCAAGGTTTTGAGGACATCGGGTGCCCGGGGC 2513
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2514 ACAGTCATCGTCCCTTTTAGGACAGTAGAAGGAACAGCCAAGGGTGGTGGTGAGGACTTT 2573

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Qy       1963 GGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG 2022
             |||||||||| |||||||| |||||||||||||||||||||||||||| ||| |||
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Qy       2263 TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC 2322
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Qy       2323 TGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCT 2382
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Qy       2383 GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC 2442
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Qy       2443 ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG 2502
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Db       3294 ATTGGCAATGTCACCGGCAGTAATGCTGTCAATGTCTTCCTGGGTATTGGTTTGGCCTGG 3353
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Qy       2503 TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA 2562
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Db       3354 TCCGTCGCCGCCATCTACTGGGCCATGCAGGGACAGGAGTTCCATGTGTCCGCTGGCACT 3413

Qy       2563 CTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG 2622
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Db       3414 CTGGCCTTCTCGGTCACTCTTTTCACCATCTTTGCATTTGTCTGCCTCAGTGTGCTCTTG 3473

Qy       2623 TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC 2682
             |||||  ||||||| |||||||| |||||||||| || || ||||||||||||| |||
Db       3474 TACCGTCGGCGGCCCCACCTGGGCGGGGAGCTTGGAGGTCCTCGTGGCTGCAAGCTTGCC 3533

Qy       2683 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2742
             ||||| |||||||||||||||||||||||||||| |||||||||||| || ||||||
Db       3534 ACAACGTGGCTCTTTGTGAGCCTGTGGCTCCTCTACGTACTCTTTGCCACGCTGGAGGCC 3593

Qy       2743 TATTGCTACATCAAGGGGTTCTAA 2766
             || |||||||||||||||||| |
Db       3594 TACTGCTACATCAAGGGGTTCTGA 3617


RESULT 13
HSA508602
LOCUS       HSA508602               3838 bp    mRNA    linear   PRI 20-JAN-2003
DEFINITION  Homo sapiens partial mRNA for Na+/Ca2+ exchanger isoform 4 (NACAIS4
            gene).
ACCESSION   AJ508602
VERSION     AJ508602.1  GI:27805124
KEYWORDS    Na+/Ca2+ exchanger isoform 4; NACAIS4 gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lindgren,R.M., Bongcam-Rudloff,E., Nister,M. and Heller,S.
  TITLE     Homo sapiens partial mRNA for Na+/Ca2+ exchanger isoform 4
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3838)
  AUTHORS   Bongcam-Rudloff,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-SEP-2002) Bongcam-Rudloff E., Animal Genetics-SLU,
            Linnaeus Centre for Bioinformatics, Box 598, 75123 Uppsala, SWEDEN
FEATURES             Location/Qualifiers
     source          1. .3838
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ORIGIN

Query Match 83.6%; Score 2312.8; DB 9; Length 3838;
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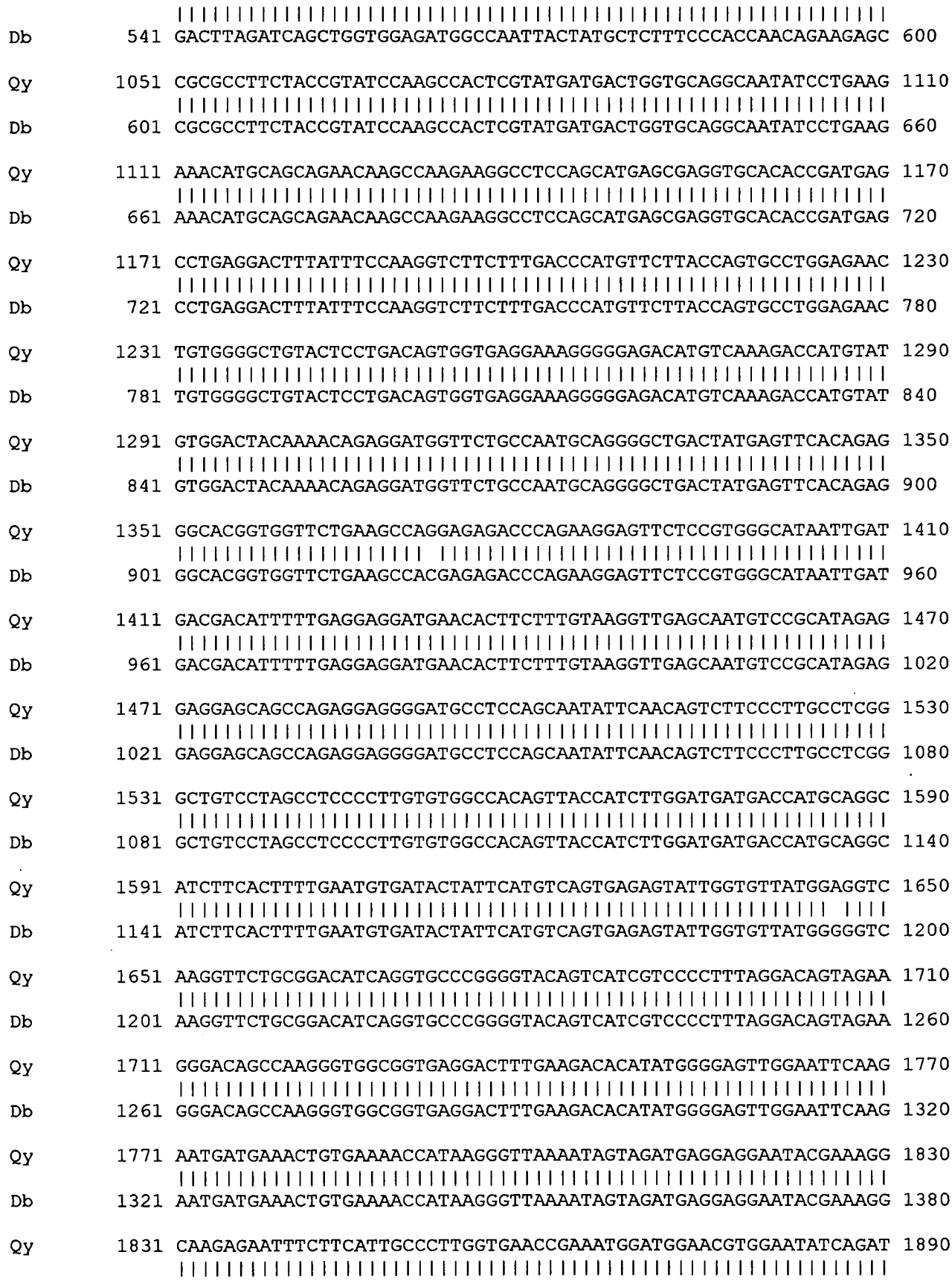

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Qy       2191 GTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCCCACAGAGTACTGCCACGGCTGGGCC 2250
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RESULT 14
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DEFINITION  Mus musculus sodium/calcium exchanger (Slc8a3) mRNA, complete cds.
ACCESSION   AF453257
VERSION     AF453257.1  GI:17432810
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3435)
  AUTHORS   Kraev,A.
  TITLE     Towards complete inventory of calcium transporters of the house
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3435)
  AUTHORS   Kraev,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-NOV-2001) Mt. Sinai Hospital, Samuel Lunenfeld
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ORIGIN

Query Match 82.8%; Score 2290.2; DB 10; Length 3435;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 2488; Conservative 0; Mismatches 278; Indels 21; Gaps 1;

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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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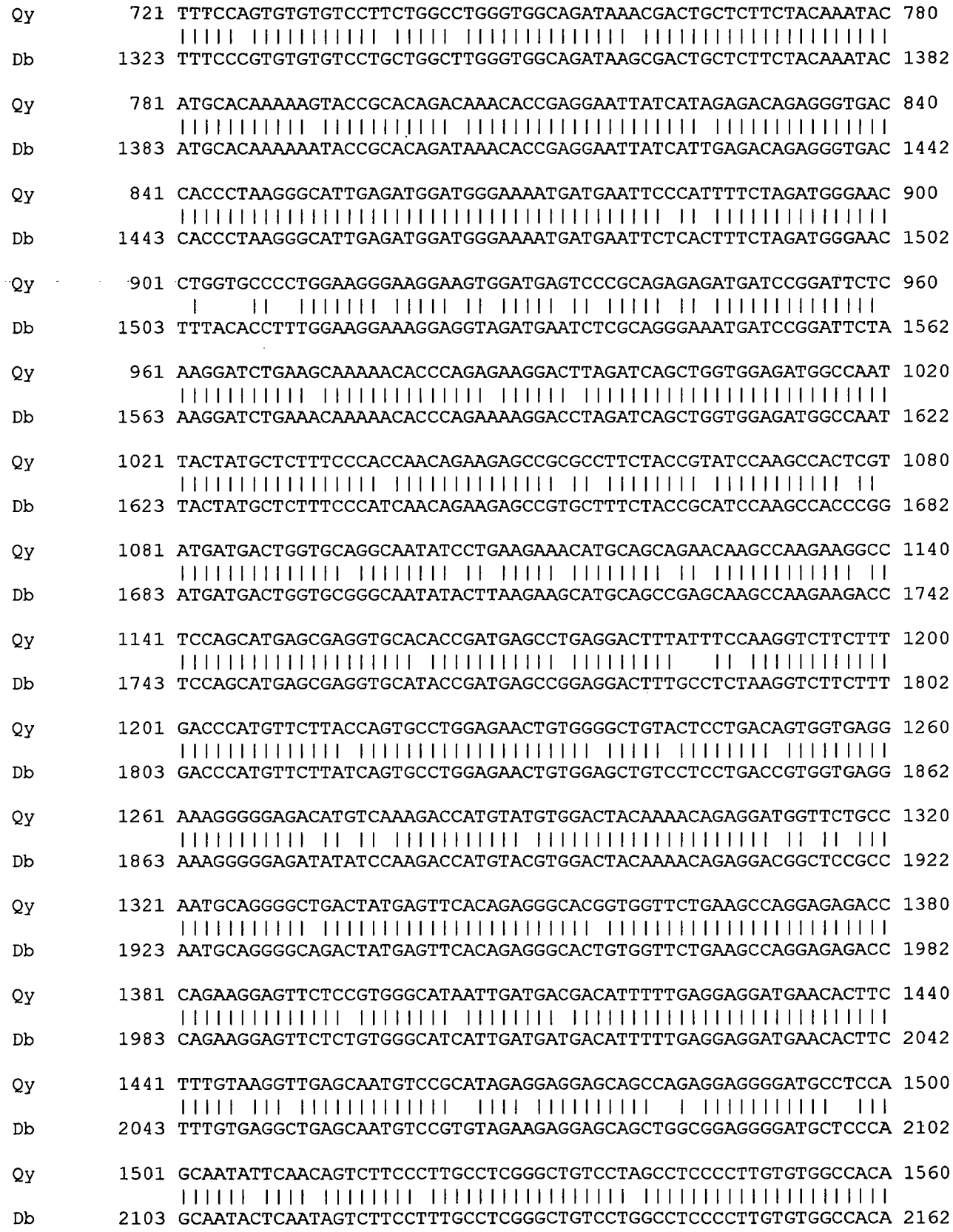

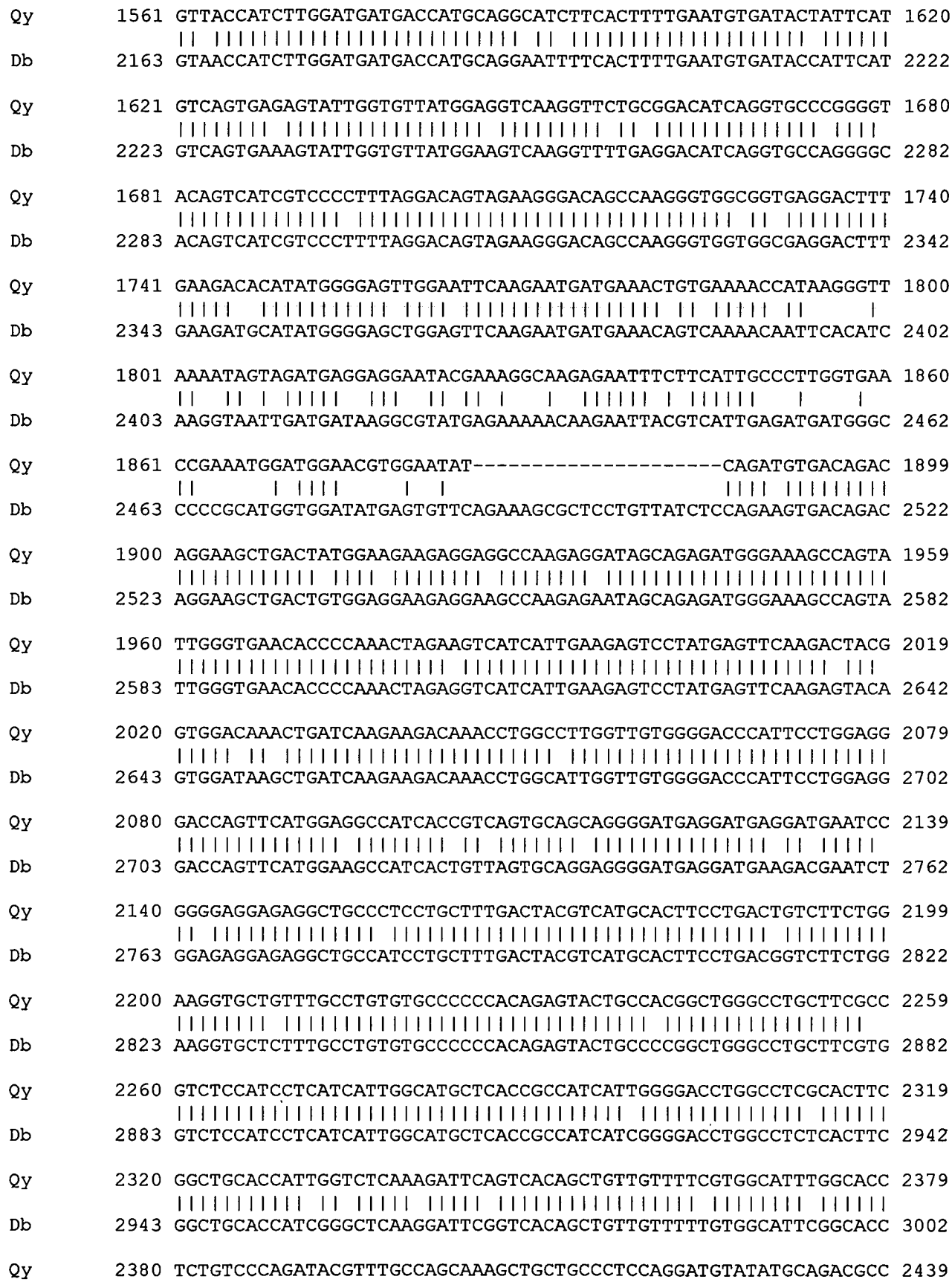

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RESULT 15
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DEFINITION  Homo sapiens partial SCL8A3 gene for solute carrier family 8
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ACCESSION   X93017
VERSION     X93017.1  GI:1067133
KEYWORDS    SLC8A3 gene; sodium-calcium exchanger.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Kraev,A., Chumakov,I. and Carafoli,E.
  TITLE     The organization of the human gene NCX1 encoding the sodium-calcium
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  JOURNAL   Genomics 37 (1), 105-112 (1996)
  MEDLINE   97079665
   PUBMED   8921376
REFERENCE   2  (bases 1 to 2534)
  AUTHORS   Kraev,A.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-1995) A.S. Kraev, Swiss Federal Institute of
            Technology, Laboratory of Biochemistry III, Universitaetstr. 16,
            Zurich, CH-8092, SWITZERLAND
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ORIGIN

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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db        1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy        1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db        1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy        1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy        1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy        1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db        1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy        1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db        2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy        1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788
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Db        2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGTAA 2130
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Search completed: June 25, 2004, 12:31:10
Job time : 10422.3 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 00:42:04 ; Search time 970.401 Seconds
(without alignments)
12108.934 Million cell updates/sec

Title: US-10-054-680-1
Perfect score: 2766
Sequence: 1 atggcgtggttaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2766	100.0	2766	6	ABQ78861	Abq78861 Human ion
2	2766	100.0	3812	6	ABQ78863	Abq78863 Human ion
3	2764.4	99.9	2766	6	ABQ78864	Abq78864 Human ion
4	2764.4	99.9	2966	6	ABZ33735	Abz33735 Human TRI
5	2761.2	99.8	2782	6	ABN83428	Abn83428 Human tra
6	2753	99.5	2769	6	ABQ78865	Abq78865 Human ion
7	2751.4	99.5	2769	6	ABQ78866	Abq78866 Human ion

	8	2733.4	98.8	2781	6	ABA04756	Aba04756 Human nat
	9	2673.2	96.6	2685	7	ABX56263	Abx56263 Human NOV
	10	2657.6	96.1	2840	7	ABX56262	Abx56262 Human NOV
	11	2367.2	85.6	2813	7	ABX56261	Abx56261 Human NOV
	12	1786.4	64.6	2534	7	ACC00414	Acc00414 Human 690
	13	1784.8	64.5	126512	6	ABN83429	Abn83429 Human tra
	14	1784.6	64.5	1863	6	ABQ78862	Abq78862 Human ion
	15	1326.4	48.0	2814	4	AAH57377	Aah57377 Human hea
	16	1294.4	46.8	3037	9	ADB59225	Adb59225 Toxicity-
	17	1277	46.2	4282	8	AAL55587	Aal55587 Human 465
	18	1277	46.2	4291	3	AAC75706	Aac75706 Human ORF
	19	1227.8	44.4	4087	6	AAD24450	Aad24450 Bovine NC
	20	1208.8	43.7	5438	5	ABV24305	Abv24305 Human pro
	21	897.4	32.4	1187	5	AAS90968	Aas90968 DNA encod
	22	897.4	32.4	1187	7	ACD05939	Acd05939 Novel hum
	23	787.2	28.5	1836	4	AAI19464	Aai19464 Probe #93
	24	787.2	28.5	1836	4	ABA64480	Aba64480 Human foe
	25	787.2	28.5	1836	4	AAI44657	Aai44657 Probe #13
	26	787.2	28.5	1836	4	ABA31619	Aba31619 Probe #10
	27	787.2	28.5	1836	4	AAK12937	Aak12937 Human bra
	28	787.2	28.5	1836	4	ABS38231	Abs38231 Human liv
	29	787.2	28.5	1836	6	ABS12734	Abs12734 Human gen
	30	593.2	21.4	4546	4	ABL09809	Abl09809 Drosophil
c	31	363	13.1	363	4	AAI85824	Aai85824 Human pol
	32	319	11.5	24221	4	ABL09808	Abl09808 Drosophil
c	33	219.4	7.9	381	4	AAI11264	Aai11264 Probe #11
c	34	219.4	7.9	381	4	ABA52926	Aba52926 Human foe
c	35	219.4	7.9	381	4	AAI32530	Aai32530 Probe #12
c	36	219.4	7.9	381	4	ABA42496	Aba42496 Human bre
c	37	219.4	7.9	381	4	ABA22706	Aba22706 Probe #11
c	38	219.4	7.9	381	4	AAK26636	Aak26636 Human bon
c	39	219.4	7.9	381	4	AAK01175	Aak01175 Human bra
c	40	219.4	7.9	381	4	ABS26227	Abs26227 Human liv
c	41	219.4	7.9	381	5	AAI01178	Aai01178 Probe #11
c	42	219.4	7.9	381	6	ABS01229	Abs01229 Human gen
	43	198.8	7.2	458	4	AAH98605	Aah98605 Rat EST-d
	44	198	7.2	325	5	ABA11549	Aba11549 Human ner
	45	186.4	6.7	491	4	AAI10735	Aai10735 Probe #66

ALIGNMENTS

RESULT 1
ABQ78861
ID ABQ78861 standard; cDNA; 2766 BP.
XX
AC ABQ78861;
XX
DT 09-OCT-2002 (first entry)
XX
DE Human ion exchanger protein #1 cDNA.
XX
KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; chromosome 14.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2766
FT /*tag= a
FT /product= "Ion exchanger protein 1"
XX
PN WO200259316-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
DR P-PSDB; ABB81913.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Claim 1; Page 36-37; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention
XX
SQ Sequence 2766 BP; 655 A; 678 C; 760 G; 673 T; 0 U; 0 Other;

Query Match 100.0%; Score 2766; DB 6; Length 2766;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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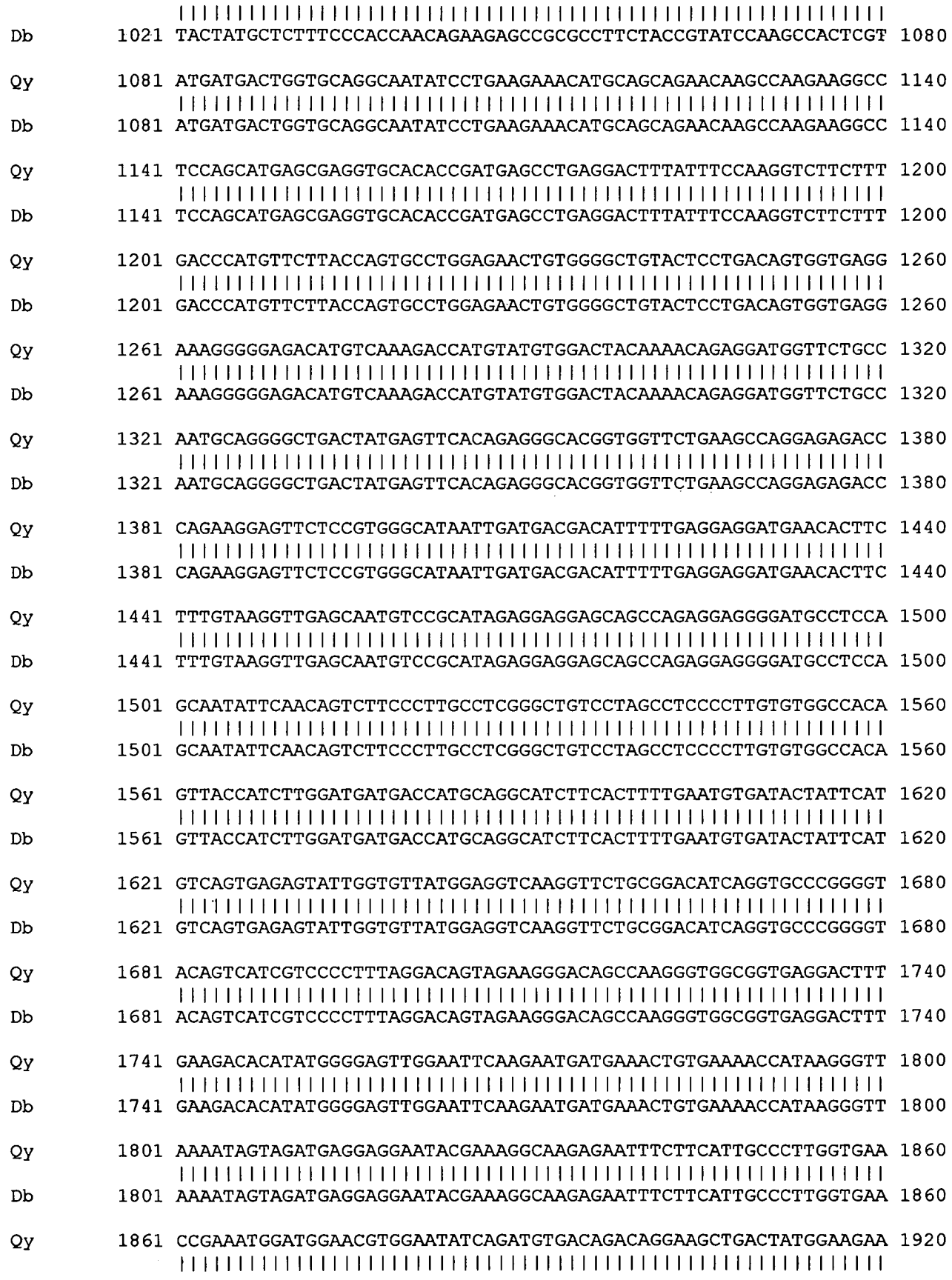

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Db       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920

Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Db       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040

Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
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Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Db       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Db       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
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Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
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Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
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Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Qy       2761 TTCTAA 2766
              ||||||
Db       2761 TTCTAA 2766


RESULT 2
ABQ78863
ID   ABQ78863 standard; cDNA; 3812 BP.
XX
AC   ABQ78863;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein cDNA #3.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; chromosome 14.
XX
OS   Homo sapiens.
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ,  Hilbun E;
XX
DR   WPI; 2002-599791/64.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page 41-42; 42pp; English.
XX
CC   The invention relates to a novel human ion exchanger protein (NHIEP),
CC   that shares structural similarity with mammalian sodium-calcium exchanger
CC   proteins, and potassium dependent versions of the same. The NHIEP of the
CC   invention has nootropic, cytostatic, antiarthritic, and virucide
CC   activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC   be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC   or to therapeutically augment the efficacy of chemotherapeutic agents
CC   used in the treatment of cancer, arthritis, or as antiviral agents. The
CC   sequence encodes a NHIEP of the invention, with regions of flanking
CC   sequence
XX
SQ   Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 2766;  DB 6;  Length 3812;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1398 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1458 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1518 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1638 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1698 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1758 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1817

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1818 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1877

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       1878 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1937

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1938 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       2118 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2177

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       2178 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       2238 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2297
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Db       2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 2417

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Db       2418 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 2477

Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Db       2478 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 2537

Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
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Db       2538 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 2597

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Db       2718 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2777

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2778 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2837

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Db       2838 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2897

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
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Db       2898 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2957

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2958 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 3017

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Db       3018 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 3077

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Db       3078 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 3137
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Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
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Db       3138 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 3197

Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
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Db       3198 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257

Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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Db       3258 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Db       3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy       2761 TTCTAA 2766
             ||||||
Db       3378 TTCTAA 3383
```

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RESULT 3
ABQ78864
ID   ABQ78864 standard; cDNA; 2766 BP.
XX
AC   ABQ78864;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein #1 cDNA A/G mutant.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1889,A)
FT                   /*tag=  a
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ,  Hilbun E;
XX
DR   WPI; 2002-599791/64.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
```

PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ Sequence 2766 BP; 654 A; 678 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 99.9%; Score 2764.4; DB 6; Length 2766;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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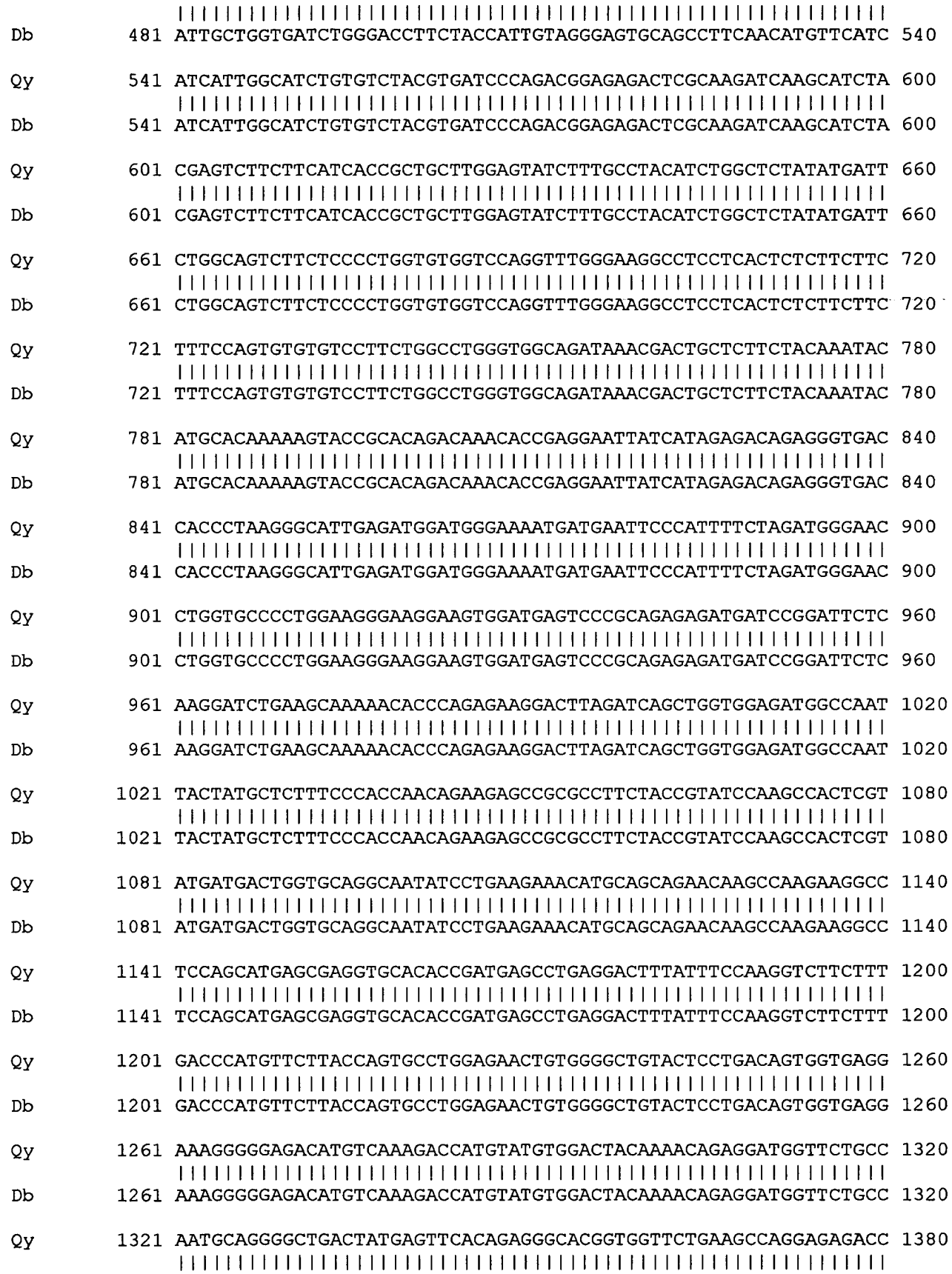

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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800

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Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1861 CCGAAATGGATGGAACGTGGAATATCAGGTGTGACAGACAGGAAGCTGACTATGGAAGAA 1920

Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040

Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100

Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520

Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580

Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640

Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760

Qy       2761 TTCTAA 2766
             ||||||
Db       2761 TTCTAA 2766
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RESULT 4
ABZ33735
ID ABZ33735 standard; cDNA; 2966 BP.
XX
AC ABZ33735;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human TRICH encoding cDNA SEQ ID NO 41.
XX
KW Human; TRICH; transporter and ion channel; transport disorder;
KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
KW neurological disorder; Alzheimer's disease; Huntington's disease;
KW immunological disorder; AIDS; asthma; cell proliferative disorder;
KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;

KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;
KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
KW hepatotropic; antiinflammatory; virucide; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200246415-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US046963.
XX
PR 08-DEC-2000; 2000US-0254303P.
PR 15-DEC-2000; 2000US-0256190P.
PR 21-DEC-2000; 2000US-0257504P.
PR 12-JAN-2001; 2001US-0261546P.
PR 19-JAN-2001; 2001US-0262832P.
PR 26-JAN-2001; 2001US-0264377P.
PR 02-FEB-2001; 2001US-0266019P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;
XX
DR WPI; 2002-519667/55.
DR P-PSDB; ABP74104.
XX
PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
PT prevention or treatment of transport, neurological, muscle, immunological
PT and cell proliferative disorders.
XX
PS Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.
XX
CC The invention relates to human transporter and ion channel polypeptide
CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
CC ABP74127), a naturally occurring polypeptide comprising a sequence having
CC at least sequence 90 % identity to (I) or a biologically active or
CC immunogenic fragment of (I). (I) is useful for screening a compound for
CC effectiveness as an agonist or antagonist, for screening a compound that
CC specifically binds (I) or modulates the activity of (I) and for preparing
CC a polyclonal or monoclonal antibody by hybridoma technology.
CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
CC screening a compound altering gene expression. (I) and (II) are useful in
CC a diagnostic tests for a condition or a disease associated with the
CC expression of TRICH in a biological sample, especially disorders selected
CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
CC Parkinson's disease, cardiac disorders, neurological disorders such as
CC Alzheimer's disease, Huntington's disease, muscle disorders,
CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
CC cancer. (II) is useful for creating knock-in humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene

CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion among normal, carrier or affected individuals and for mapping
CC genomic sequences. Note: The sequence data for this patent is not
CC represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 2966 BP; 692 A; 725 C; 809 G; 740 T; 0 U; 0 Other;

Query Match 99.9%; Score 2764.4; DB 6; Length 2966;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 260

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 320

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 380

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 440

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 500

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 560

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 620

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 680

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 740

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 800

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 860
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 920

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 980

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1040

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1041 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1100

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1101 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1160

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1161 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1220

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCCGCGCTTCTACCGTATCCAAGCCACTCGT 1080
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1221 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1280

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1281 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1340

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1341 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1400

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1401 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1460

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1461 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1520

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1521 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1580

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1581 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1640

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1641 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1700

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1701 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1760

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1761 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1820

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1821 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1880

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1881 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1940

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1941 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 2000

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2001 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 2060

Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2061 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 2120

Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2121 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 2180

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2181 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2240

Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2241 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2300

Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2301 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2360

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2361 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2420

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2421 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2480

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2481 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2540

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2541 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2600

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2601 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2660

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2661 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2720

Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2721 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2780

Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2781 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2840

Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2841 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2900

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2901 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2960

Qy       2761 TTCTAA 2766
              ||||||
Db       2961 TTCTAA 2966
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RESULT 5
ABN83428
ID   ABN83428 standard; cDNA; 2782 BP.
XX
AC   ABN83428;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Human transporter protein coding sequence.
XX
KW   Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW   spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             10. .2775
FT                   /*tag=  a
FT                   /product= "Human transporter"
XX
PN   WO200233086-A2.
XX
PD   25-APR-2002.
XX
PF   17-OCT-2001; 2001WO-US032152.
XX
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PR 17-OCT-2000; 2000US-0240836P.
PR 13-MAR-2001; 2001US-00804474.
XX
PA (PEKE) PE CORP NY.
XX
PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;
PI Beasley EM;
XX
DR WPI; 2002-479677/51.
DR P-PSDB; ABB83246.
XX
PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein.
XX
PS Claim 4; Fig 1; 200pp; English.
XX
CC The present sequence is the coding sequence of a human transporter
CC protein, which is related to the sodium/calcium exchanger subfamily.
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR
XX
SQ Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

Query Match 99.8%; Score 2761.2; DB 6; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC 969

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy        1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy        1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy        1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy        1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy        1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy        1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy        1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy        1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1809

Qy        1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1810 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1869

Qy        1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1870 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1929

Qy        1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1930 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTG 1989

Qy        1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1990 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2049

Qy        2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2050 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2109

Qy        2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2110 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2169

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2229

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2289

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2349

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GATTCGGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2409

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2469

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2529

Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2589

Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2649

Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2709

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2769

Qy       2761 TTCTAA 2766
             ||||||
Db       2770 TTCTAA 2775
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RESULT 6
ABQ78865
ID ABQ78865 standard; cDNA; 2769 BP.
XX
AC ABQ78865;
XX
DT 09-OCT-2002 (first entry)
XX
DE Human ion exchanger protein #1 cDNA GCA mutant.
XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(2113. .2115,-)
FT /*tag= a
XX
PN WO200259316-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ Sequence 2769 BP; 656 A; 679 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 99.5%; Score 2753; DB 6; Length 2769;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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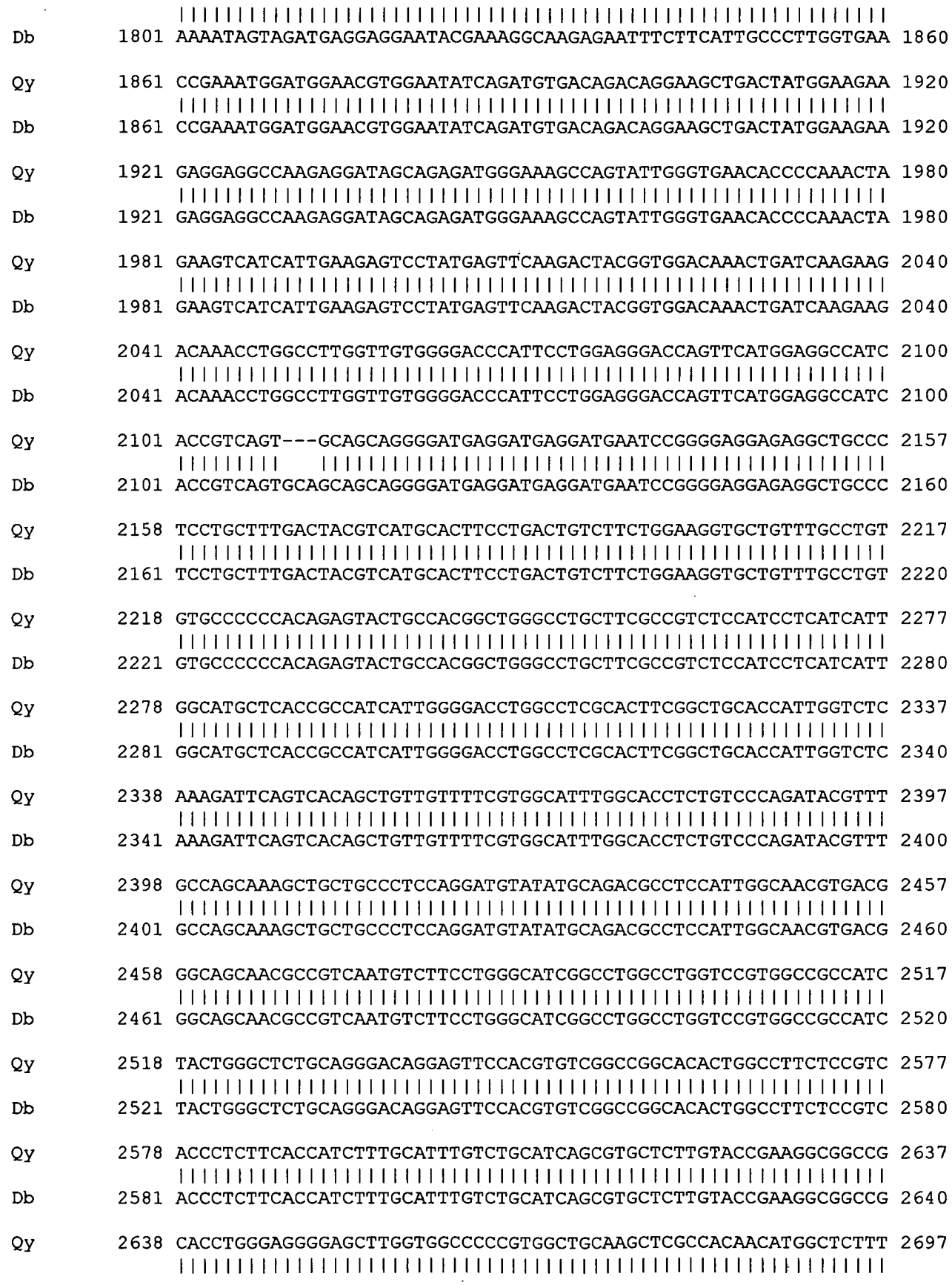

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Db       2701 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2760

Qy       2758 GGGTTCTAA 2766
              |||||||||
Db       2761 GGGTTCTAA 2769


RESULT 7
ABQ78866
ID   ABQ78866 standard; cDNA; 2769 BP.
XX
AC   ABQ78866;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein #1 cDNA A/G+GCA mutant.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1889,A)
FT                   /*tag=  a
FT   mutation        replace(2113. .2115,-)
FT                   /*tag=  b
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ,  Hilbun E;
XX
DR   WPI; 2002-599791/64.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page; 42pp; English.
XX
CC   The invention relates to a novel human ion exchanger protein (NHIEP),
CC   that shares structural similarity with mammalian sodium-calcium exchanger
```

CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ Sequence 2769 BP; 655 A; 679 C; 762 G; 673 T; 0 U; 0 Other;

Query Match 99.5%; Score 2751.4; DB 6; Length 2769;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2765; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860

Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
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Db       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980

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Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2101 ACCGTCAGT---GCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC 2157
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ACCGTCAGTGCAGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCC 2160

Qy       2158 TCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGT 2217
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Qy       2218 GTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATT 2277
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Qy       2278 GGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTC 2337
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Qy       2338 AAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTT 2397
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Qy       2398 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG 2457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACG 2460

Qy       2458 GGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC 2517
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Qy       2518 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTC 2577
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Db       2521 TACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTC 2580

Qy       2578 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG 2637
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Db       2581 ACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCG 2640

Qy       2638 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2697
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Db       2641 CACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTT 2700

Qy       2698 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2757
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Db       2701 GTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAG 2760

Qy       2758 GGGTTCTAA 2766
             |||||||||
Db       2761 GGGTTCTAA 2769
```

```
RESULT 8
ABA04756
ID   ABA04756 standard; cDNA; 2781 BP.
XX
AC   ABA04756;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.
XX
KW   Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
KW   cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
KW   myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
KW   coronary heart disease; renal failure; ischaemic disorder;
KW   Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2781
FT                   /*tag=  a
FT                   /partial
FT                   /product= "Human natrium(+)-calcium(2+) exchanger form 3
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FT protein, HNCX3"
FT /note= "No stop codon given"
XX
PN WO200183744-A2.
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-EP004886.
XX
PR 02-MAY-2000; 2000EP-00109080.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Wilm C;
XX
DR WPI; 2002-041493/05.
DR P-PSDB; AAM47745.
XX
PT New polypeptide, useful as vaccines for inducing immune response against
PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
PT renal disorders in mammal.
XX
PS Claim 4; Page 34-38; 41pp; English.
XX
CC The present sequence is the coding sequence for human Natrium(+)-Calcium
CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC 14. HNCX3 and its coding sequence are useful for treating acute and
CC chronic cardiac failure of different aetiologies, myocardial infarction,
CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC and ischaemic brain disorders of different aetiologies
XX
SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 U; 0 Other;

Query Match 98.8%; Score 2733.4; DB 6; Length 2781;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

```
Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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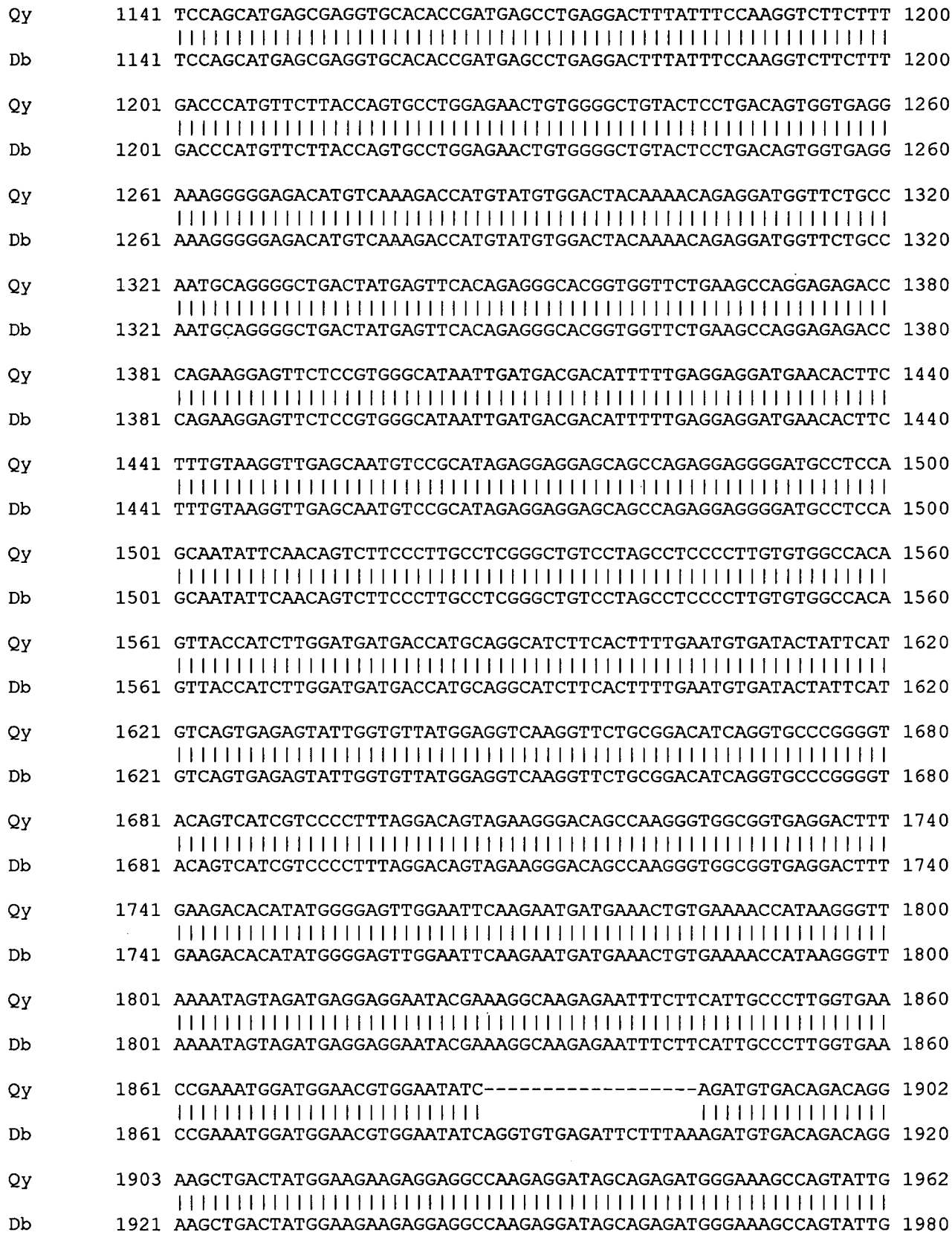

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Qy       1963 GGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG 2022
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Db       1981 GGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG 2040

Qy       2023 GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGAC 2082
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Db       2041 GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGAC 2100

Qy       2083 CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG 2142
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Db       2101 CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG 2160

Qy       2143 GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG 2202
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Db       2161 GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG 2220

Qy       2203 GTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC 2262
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Qy       2263 TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC 2322
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Qy       2323 TGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCT 2382
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Qy       2383 GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC 2442
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Qy       2443 ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG 2502
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Qy       2503 TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA 2562
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Qy       2563 CTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG 2622
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Qy       2623 TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC 2682
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Db       2641 TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC 2700

Qy       2683 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2760

Qy       2743 TATTGCTACATCAAGGGGTTC 2763
             |||||||||||||||||||||
Db       2761 TATTGCTACATCAAGGGGTTC 2781
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RESULT 9
ABX56263
ID ABX56263 standard; DNA; 2685 BP.
XX
AC ABX56263;
XX
DT 19-FEB-2003 (first entry)
XX
DE Human NOV1c 248057963 DNA SEQ ID 5.
XX
KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease; ds.
XX
OS Homo sapiens.
XX
PN WO200281625-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010366.
XX
PR 03-APR-2001; 2001US-0281086P.
PR 05-APR-2001; 2001US-0281906P.
PR 06-APR-2001; 2001US-0282020P.
PR 10-APR-2001; 2001US-0282930P.
PR 12-APR-2001; 2001US-0283444P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 24-APR-2001; 2001US-0286068P.
PR 25-APR-2001; 2001US-0286292P.
PR 07-JUN-2001; 2001US-0296692P.
PR 26-JUN-2001; 2001US-0300883P.
PR 08-AUG-2001; 2001US-0311003P.
PR 13-AUG-2001; 2001US-0311973P.
PR 16-AUG-2001; 2001US-0312901P.
PR 14-SEP-2001; 2001US-0322283P.
PR 05-OCT-2001; 2001US-0327448P.
PR 31-DEC-2001; 2001US-0345734P.
PR 03-JAN-2002; 2002US-0345755P.
PR 04-FEB-2002; 2002US-0354391P.
PR 02-APR-2002; 2002US-00114153.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;

PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;
XX
DR WPI; 2003-046862/04.
DR P-PSDB; ABU12043.
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Claim 3; Page 85-86; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
XX
SQ Sequence 2685 BP; 645 A; 657 C; 741 G; 642 T; 0 U; 0 Other;

Query Match 96.6%; Score 2673.2; DB 7; Length 2685;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2675; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy         86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 145
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Db          2 GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 61

Qy        146 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 205
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Qy        206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
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Qy        266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
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Qy       386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 445
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Qy       446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 505
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Qy       506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 565
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Qy       566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
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Db       482 TCCCAGACGGAGAGACTCGCAAGATCAAACATCTACGAGTCTTCTTCATCACCGCTGCTT 541

Qy       626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
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Qy       686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745
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Qy       746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
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Qy       866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 925
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Qy       926 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 985
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Qy       986 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 1045
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Qy      1046 AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1105
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Qy      1106 TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG 1165
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Qy      1166 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1225
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Qy       1226 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1285
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Db       1142 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1201

Qy       1286 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1345
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1261

Qy       1346 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA 1405
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Qy       1406 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1465
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Db       1322 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1381

Qy       1466 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1525
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Qy       1526 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1585
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Qy       1586 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1645
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Qy       1706 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1765
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Qy       1766 TCAAGAATGATGAAACTGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAATACG 1825
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Qy       1826 AAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAACCGAAATGGATGGAACGTGGAATAT 1885
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Qy       1886 CAGATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1945
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Qy       1946 TGGGAAAGCCAGTATTGGGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATG 2005
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 TGGGAAAGCCAGTATTGGGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATG 1921

Qy       2006 AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA 2065
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1922 AGTTCAAGACTACGGTGGACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGA 1981

Qy       2066 CCCATTCCTGGAGGGACCAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGG 2125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2126 ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC 2185
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Db       2042 ATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCC 2101

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Db       2222 TGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCG 2281

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Db       2342 TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG 2401

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Qy       2546 ACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCT 2605
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Db       2462 ACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCT 2521

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Qy       2666 GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT 2725
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RESULT 10
ABX56262
ID   ABX56262 standard; DNA; 2840 BP.
XX
AC   ABX56262;
XX
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DT 19-FEB-2003 (first entry)
XX
DE Human NOV1b CG56558-02 DNA SEQ ID 3.
XX
KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease; ds.
XX
OS Homo sapiens.
XX
PN WO200281625-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010366.
XX
PR 03-APR-2001; 2001US-0281086P.
PR 05-APR-2001; 2001US-0281906P.
PR 06-APR-2001; 2001US-0282020P.
PR 10-APR-2001; 2001US-0282930P.
PR 12-APR-2001; 2001US-0283444P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 24-APR-2001; 2001US-0286068P.
PR 25-APR-2001; 2001US-0286292P.
PR 07-JUN-2001; 2001US-0296692P.
PR 26-JUN-2001; 2001US-0300883P.
PR 08-AUG-2001; 2001US-0311003P.
PR 13-AUG-2001; 2001US-0311973P.
PR 16-AUG-2001; 2001US-0312901P.
PR 14-SEP-2001; 2001US-0322283P.
PR 05-OCT-2001; 2001US-0327448P.
PR 31-DEC-2001; 2001US-0345734P.
PR 03-JAN-2002; 2002US-0345755P.
PR 04-FEB-2002; 2002US-0354391P.
PR 02-APR-2002; 2002US-00114153.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;
XX
DR WPI; 2003-046862/04.
DR P-PSDB; ABU12042.

XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Claim 3; Page 84; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
XX
SQ Sequence 2840 BP; 668 A; 700 C; 775 G; 697 T; 0 U; 0 Other;

Query Match 96.1%; Score 2657.6; DB 7; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        363 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 422

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Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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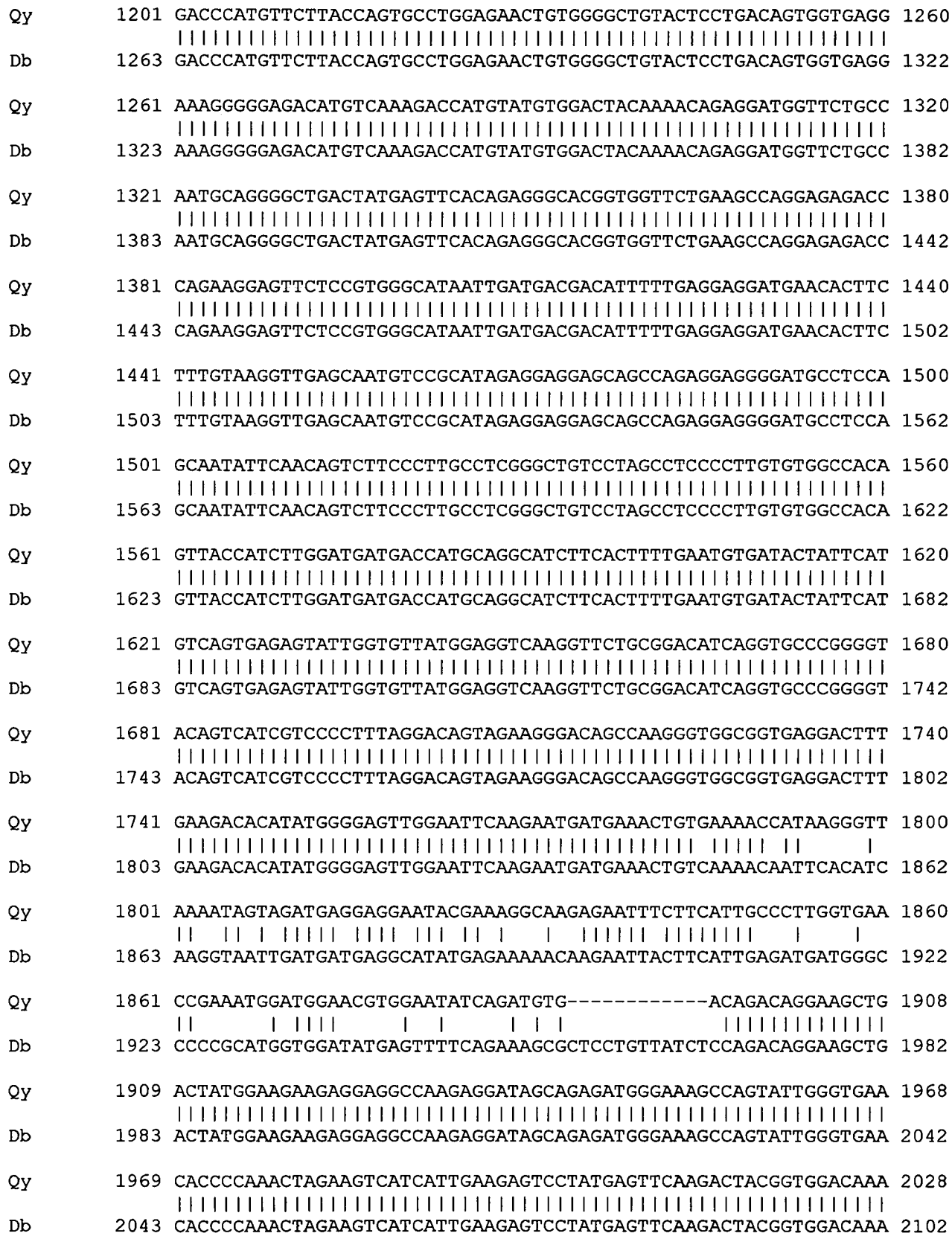
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Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db 1863 AAGGTAATTGATGATGAGGCATATGAGAAAAACAAGAATTACTTCATTGAGATGATGGGC 1922
Qy 1861 CCGAAATGGATGGAACGTGGAATATCAGATGTG----------ACAGACAGGAAGCTG 1908
Db 1923 CCCCGCATGGTGGATATGAGTTTTCAGAAAGCGCTCCTGTTATCTCCAGACAGGAAGCTG 1982
Qy 1909 ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA 1968
Db 1983 ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA 2042
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Qy       2749 TACATCAAGGGGTTCTAA 2766
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Db       2823 TACATCAAGGGGTTCTAA 2840


RESULT 11
ABX56261
ID   ABX56261 standard; DNA; 2813 BP.
XX
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AC ABX56261;
XX
DT 19-FEB-2003 (first entry)
XX
DE Human NOV1a CG56258-01 DNA SEQ ID 1.
XX
KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease; ds.
XX
OS Homo sapiens.
XX
PN WO200281625-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010366.
XX
PR 03-APR-2001; 2001US-0281086P.
PR 05-APR-2001; 2001US-0281906P.
PR 06-APR-2001; 2001US-0282020P.
PR 10-APR-2001; 2001US-0282930P.
PR 12-APR-2001; 2001US-0283444P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 24-APR-2001; 2001US-0286068P.
PR 25-APR-2001; 2001US-0286292P.
PR 07-JUN-2001; 2001US-0296692P.
PR 26-JUN-2001; 2001US-0300883P.
PR 08-AUG-2001; 2001US-0311003P.
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PR 02-APR-2002; 2002US-00114153.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
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XX

DR WPI; 2003-046862/04.
DR P-PSDB; ABU12041.
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Claim 3; Page 83-84; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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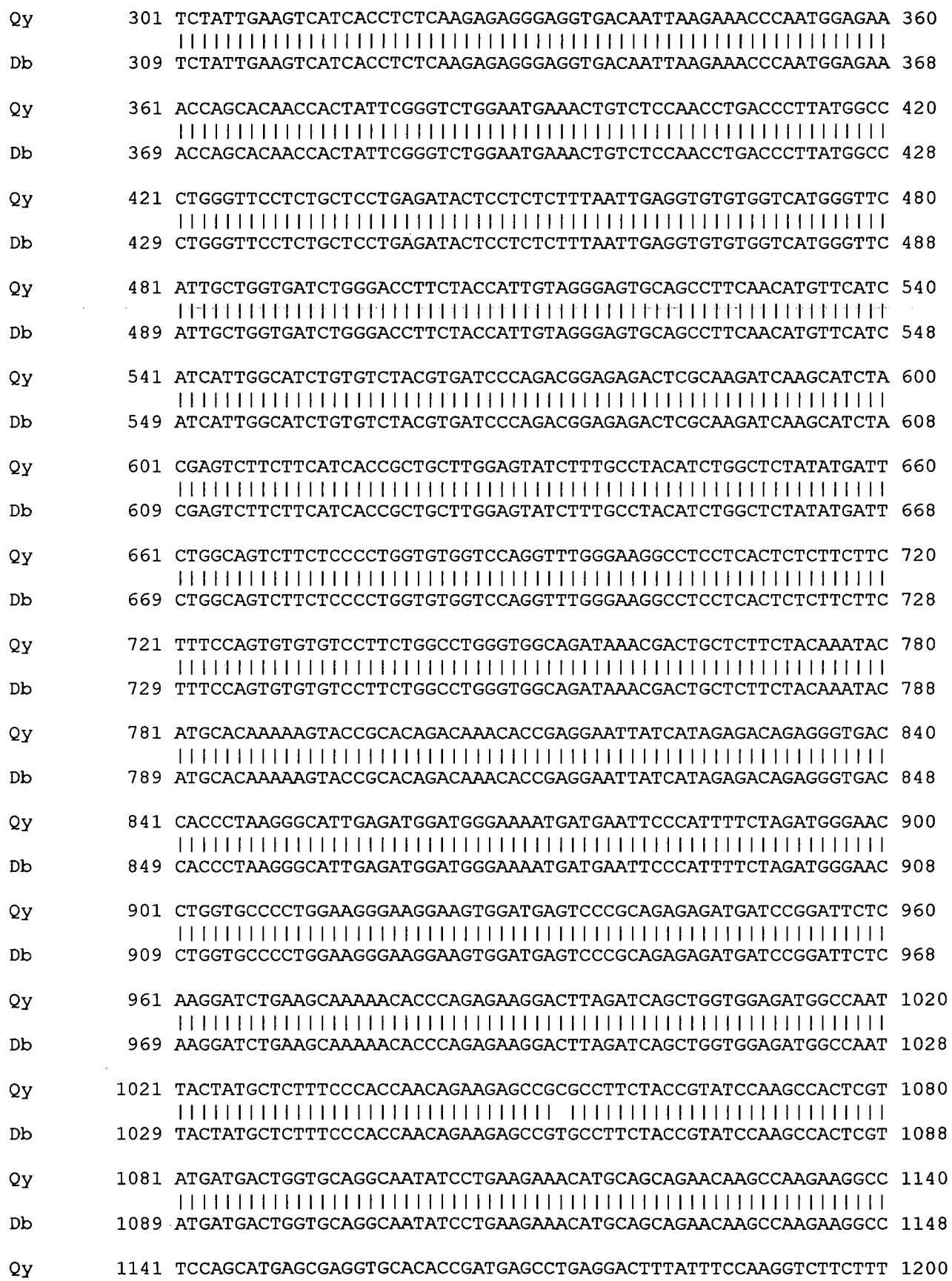

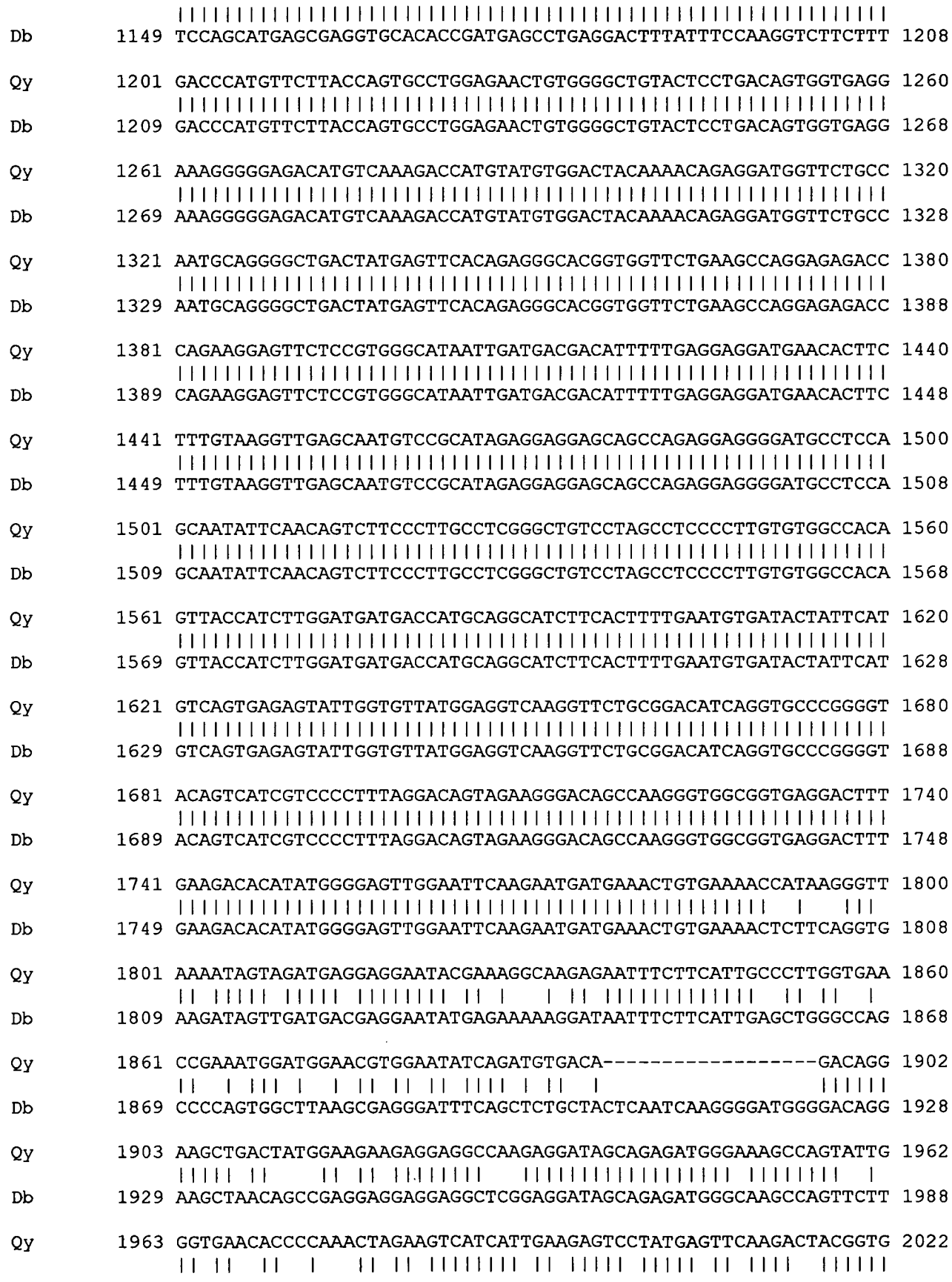

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Qy       2083 CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAA---TCC 2139
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Db       2229 AAGGTGCTCTTCGCCTGTGTGCCCCCCACCGAGTACTGCCACGGCTGGGCCTGCTTTGGT 2288

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Qy       2320 GGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACC 2379
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Qy       2380 TCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCC 2439
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Qy       2500 TGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGC 2559
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RESULT 12
ACC00414
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ID ACC00414 standard; cDNA; 2534 BP.
XX
AC ACC00414;
XX
DT 04-JUL-2003 (first entry)
XX
DE Human 69039 coding sequence.
XX
KW Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;
KW Na+/Ca2+ exchanger; ion transporter; neural tissue;
KW neurological disorder; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   343. .2130
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PN WO2003029410-A2.
XX
PD 10-APR-2003.
XX
PF 27-SEP-2002; 2002WO-US030817.
XX
PR 28-SEP-2001; 2001US-0325737P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Carroll JM;
XX
DR WPI; 2003-381617/36.
DR P-PSDB; ABR40134.
XX
PT Identifying a nucleic acid molecule associated with a disorder for
PT preparing a composition for treating hematopoietic or neurological
PT disorder by detecting the presence of a nucleic acid molecule in the
PT sample that is amplified.
XX
PS Claim 1; Page 109-110; 133pp; English.
XX
CC The present sequence is the coding sequence for human 69039, a novel
CC Na+/Ca2+ exchanger family member (ion transporter). 69039 was shown to be
CC expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC 69039 may therefore be used for preparing a composition for treating
CC haematopoietic or neurological disorder
XX
SQ Sequence 2534 BP; 602 A; 595 C; 644 G; 693 T; 0 U; 0 Other;

  Query Match   64.6%; Score 1786.4; DB 7; Length 2534;
  Best Local Similarity   99.9%; Pred. No. 0;
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Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db       643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db      1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788
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RESULT 13
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AC   ABN83429;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Human transporter protein gene.
XX
KW   Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW   spleen; testis; leukocyte; foetal brain; chromosome 14; gene;
KW   single nucleotide polymorphism; SNP; ds.
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Query Match 64.5%; Score 1784.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db       2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2070 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 2189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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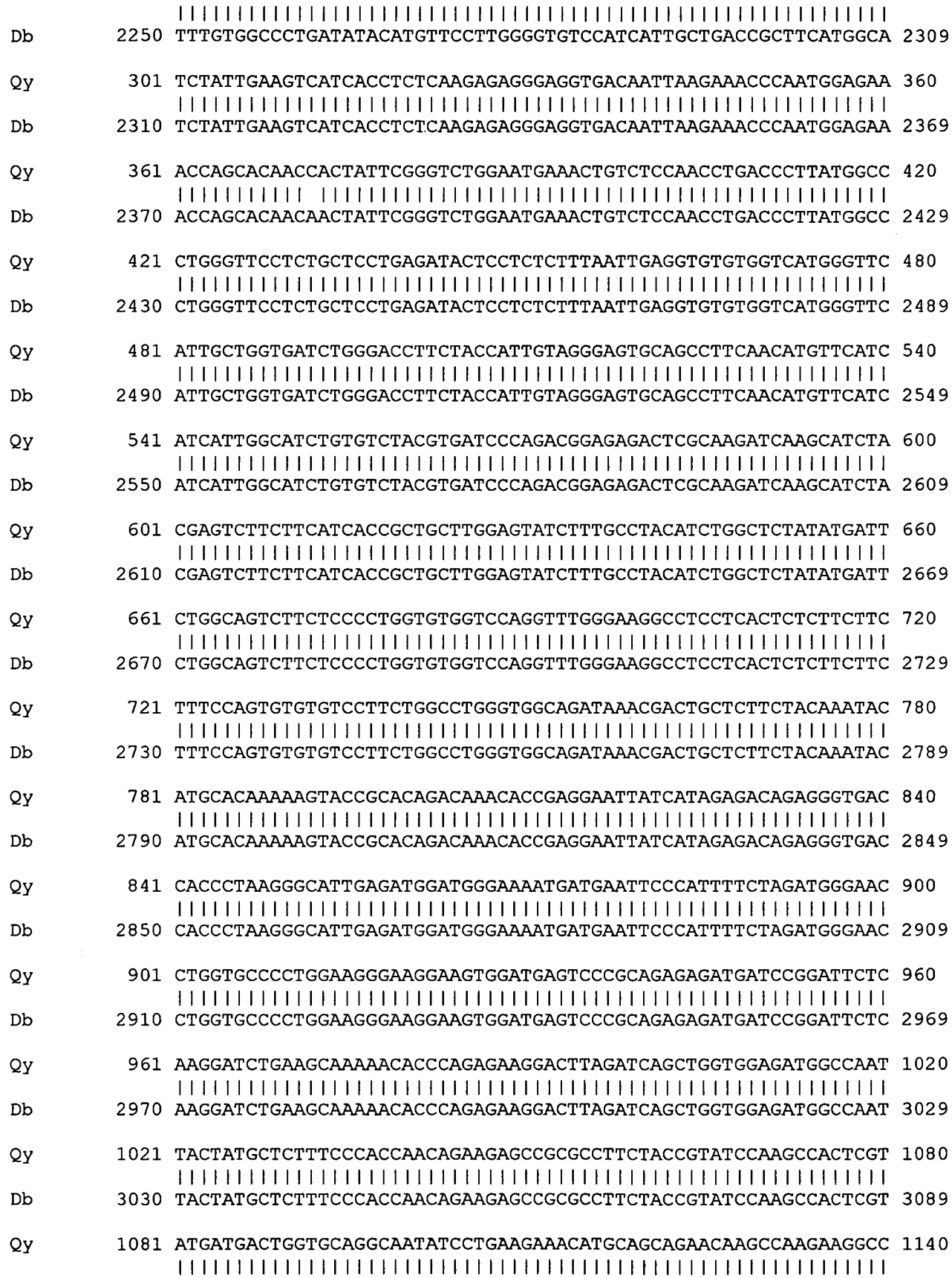

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Db       3090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 3149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 3209

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 3269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       3270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 3329

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 3389

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 3449

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 3509

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 3569

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 3689

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788
              |||||||||||||||||||||||||||||||||||||||||||||| ||
Db       3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGTAA 3797
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RESULT 14
ABQ78862
ID ABQ78862 standard; cDNA; 1863 BP.
XX
AC ABQ78862;
XX
DT 09-OCT-2002 (first entry)
XX
DE Human ion exchanger protein #2 cDNA.
XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; chromosome 14.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1863
FT /*tag= a
FT /product= "Ion exchanger protein 2"
XX
PN WO200259316-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
DR P-PSDB; ABB81914.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page 39-40; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention
XX
SQ Sequence 1863 BP; 464 A; 426 C; 514 G; 459 T; 0 U; 0 Other;

Query Match 64.5%; Score 1784.6; DB 6; Length 1863;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

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Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

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Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800

Qy       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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Db 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841

RESULT 15
AAH57377
ID AAH57377 standard; cDNA; 2814 BP.
XX
AC AAH57377;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human heart cell specific cDNA sequence SEQ ID NO:217.
XX
KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX
OS Homo sapiens.
XX
PN WO200132927-A2.
XX
PD 10-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US030396.
XX
PR 04-NOV-1999; 99US-0163508P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Sornasse T, Seilhamer JJ, Watson GA;
XX
DR WPI; 2001-291057/30.
XX
PT New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.
XX
PS Claim 1; Page 146-147; 327pp; English.
XX
CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology
XX
SQ Sequence 2814 BP; 754 A; 579 C; 718 G; 763 T; 0 U; 0 Other;

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  Query Match             48.0%;  Score 1326.4;  DB 4;  Length 2814;
  Best Local Similarity   69.8%;  Pred. No. 0;
  Matches 1893;  Conservative    0;  Mismatches  756;  Indels   63;  Gaps    5;

Qy        109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
              ||  ||  | |   |||  |  | | ||     ||| | || ||||   |||| ||| |
Db        112 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 171

Qy        169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
              || ||  ||  |||| || ||| | ||  |  |||||||  |||||||||| ||||| ||
Db        172 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 231

Qy        229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
              |  | ||| ||||||||||||| || | |||||||| ||||| || || ||||| |||||
Db        232 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 291

Qy        289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
              || |||||| | ||||| |||||||||| |||||||| |  ||  | || || ||||||
Db        292 CGGTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA 351

Qy        349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408
              |||||||||| |||| ||  || ||| |  || |||||||||||| || || ||||||
Db        352 CCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 411

Qy        409 ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468
              ||| | |||||||||||| || |||||||||||||| ||||| ||  ||||||| ||||||
Db        412 ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT 471

Qy        469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
              || |||   |||| ||| || || || || |||   ||||| || || ||||| || |||
Db        472 GGCCATAACTTCACTGCAGGAGACCTCGGTCCTAGCACCATCGTGGGAAGTGCTGCATTC 531

Qy        529 AACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588
              || |||||||||| ||||   ||||||| || ||| | || ||||||||||  | |||
Db        532 AATATGTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 591

Qy        589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG 648
              || |||||| | || ||||||||  | || || || ||||| |||||||||||| ||||
Db        592 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG 651

Qy        649 CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
              || || || ||| || | ||| | || |||||||| ||  |||| ||||||||  | ||
Db        652 CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTTGTGGAGGTCTGGGAAGGTTTGCTT 711

Qy        709 ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 768
              ||| ||||||||||||||  | |||||  |  | || ||||| || ||||   |||| ||
Db        712 ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTCGCTTGGGTAGCGGATAGGAGACTTCTG 771

Qy        769 TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 828
              || ||||| ||  |  |||| | ||| ||  | | ||| ||  | || || || || ||
Db        772 TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 831

Qy        829 ACAGAGGGTGACCACCC----------TAAGGGCATTGAGATGGATGGGAAAATGATGAAT 879
                 || || |||   ||           |  |  ||||| ||||| |||||| || | |||
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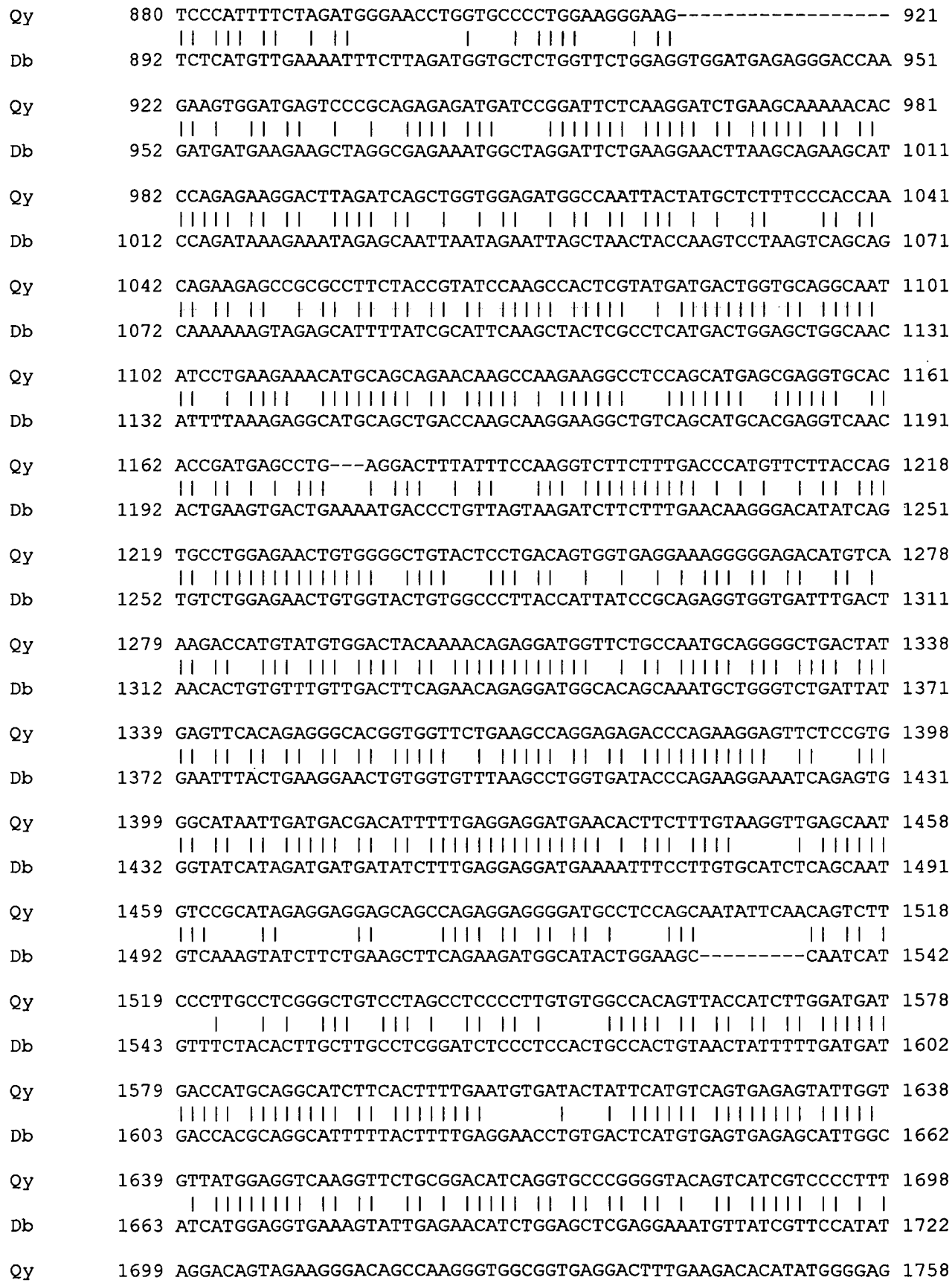

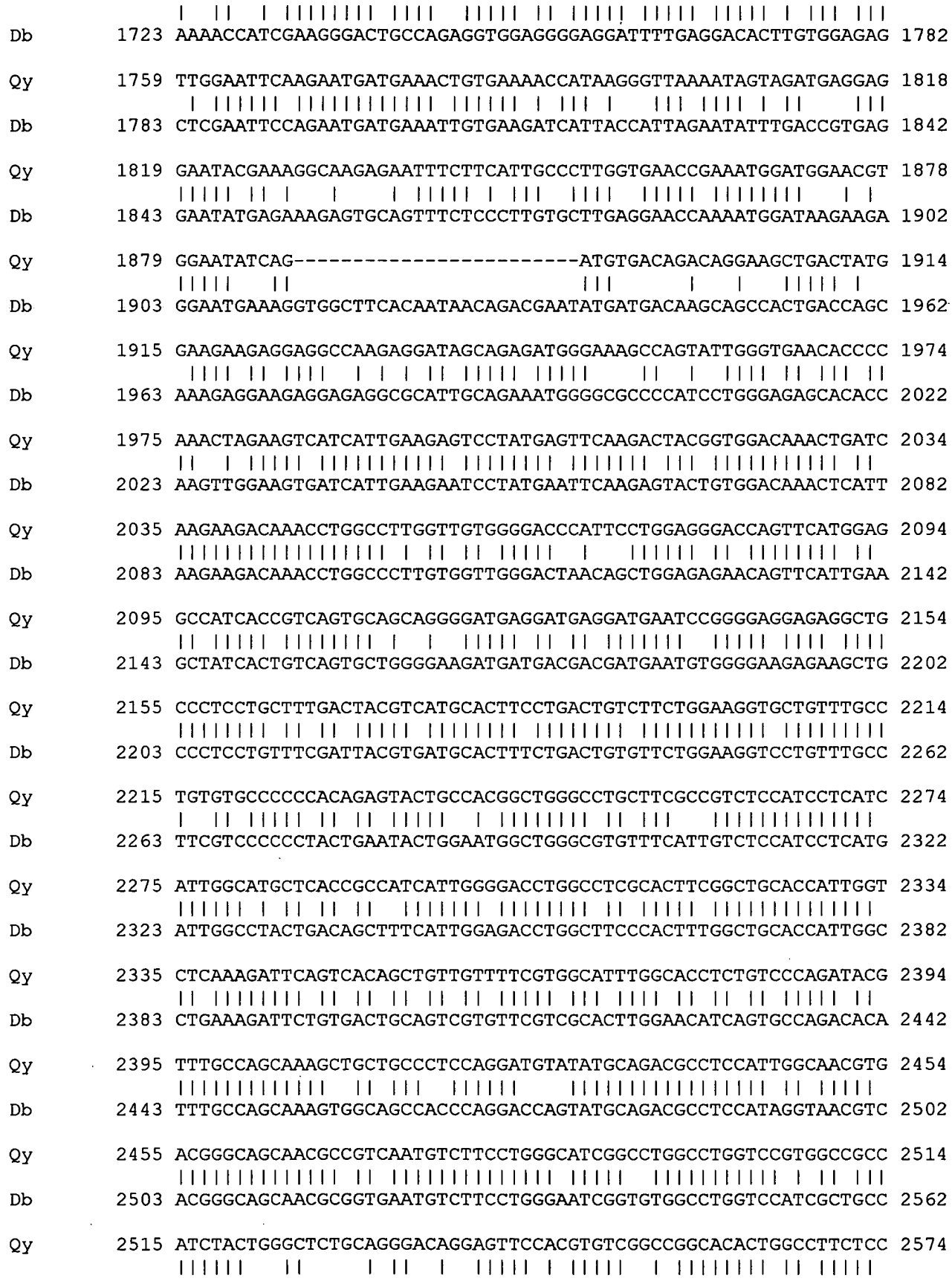

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Db       2563 ATCTACCACGCAGCCAATGGGGAACAGTTCAAAGTGTCCCCTGGCACACTAGCTTTCTCT 2622

Qy       2575 GTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGG 2634
              ||||| |||||||||||| ||||| ||  ||     |  | |||||  |||| ||  || ||
Db       2623 GTCACTCTCTTCACCATTTTTGCTTTCATCAATGTGGGGGTGCTGCTGTATCGGCGGAGG 2682

Qy       2635 CCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTC 2694
              ||  |  | ||||| ||||| ||||| |||||      |||||||  |||| | || |||
Db       2683 CCAGAAATCGGAGGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTC 2742

Qy       2695 TTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATC 2754
              ||||||  ||| |||||| | |||||  ||||  || | || |||||||| ||| ||||
Db       2743 TTTGTGCTCCTATGGCTCTTGTACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATA 2802

Qy       2755 AAGGGGTTCTAA 2766
              || || ||||||
Db       2803 AAAGGCTTCTAA 2814
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Search completed: June 25, 2004, 07:40:38
Job time : 985.401 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 06:15:36 ; Search time 210.931 Seconds
(without alignments)
7277.246 Million cell updates/sec

Title: US-10-054-680-1
Perfect score: 2766
Sequence: 1 atggcgtggttaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	78.8	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
	2	76.6	2.8	1935	4	US-09-701-068-3	Sequence 3, Appli
	3	76.6	2.8	1950	4	US-09-701-068-1	Sequence 1, Appli
	4	51.6	1.9	7218	1	US-08-232-463-14	Sequence 14, Appl
c	5	50.2	1.8	390	3	US-09-197-649-7	Sequence 7, Appli
	6	46.2	1.7	3984	4	US-09-016-434-1199	Sequence 1199, Ap
	7	46.2	1.7	4559	4	US-09-919-172-61	Sequence 61, Appl
	8	44.8	1.6	2803	4	US-09-701-068-4	Sequence 4, Appli
c	9	44.2	1.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	10	43.8	1.6	1992	4	US-09-252-991A-9693	Sequence 9693, Ap
	11	43.8	1.6	2658	4	US-09-252-991A-9558	Sequence 9558, Ap

	12	43.8	1.6	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
c	13	43.4	1.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	14	42.2	1.5	660	4	US-09-252-991A-5866	Sequence 5866, Ap
	15	42.2	1.5	1983	4	US-09-252-991A-5825	Sequence 5825, Ap
c	16	42.2	1.5	1995	4	US-09-252-991A-5783	Sequence 5783, Ap
	17	41.8	1.5	870	4	US-09-252-991A-3650	Sequence 3650, Ap
	18	41.8	1.5	1098	4	US-09-252-991A-3605	Sequence 3605, Ap
c	19	41.8	1.5	3402	4	US-09-252-991A-1374	Sequence 1374, Ap
	20	41.8	1.5	3687	4	US-09-252-991A-1193	Sequence 1193, Ap
	21	41.8	1.5	4266	4	US-09-252-991A-1234	Sequence 1234, Ap
	22	41.4	1.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	23	41.4	1.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	24	40.2	1.5	1174	3	US-09-034-985-1	Sequence 1, Appli
	25	40	1.4	570	4	US-09-252-991A-10419	Sequence 10419, A
c	26	40	1.4	789	4	US-09-252-991A-10654	Sequence 10654, A
c	27	40	1.4	813	4	US-09-252-991A-10547	Sequence 10547, A
	28	40	1.4	831	4	US-09-252-991A-10512	Sequence 10512, A
	29	39.6	1.4	3431	4	US-09-221-017B-993	Sequence 993, App
	30	39.2	1.4	333	4	US-09-252-991A-3700	Sequence 3700, Ap
c	31	39	1.4	642	4	US-09-252-991A-4949	Sequence 4949, Ap
	32	39	1.4	1617	4	US-09-489-039A-2262	Sequence 2262, Ap
	33	39	1.4	1926	4	US-09-249-585A-4	Sequence 4, Appli
	34	39	1.4	1931	2	US-09-130-114-2	Sequence 2, Appli
	35	39	1.4	1932	4	US-09-252-991A-4998	Sequence 4998, Ap
c	36	38.6	1.4	1548	2	US-08-762-106-5	Sequence 5, Appli
c	37	38.6	1.4	1548	3	US-09-320-774-5	Sequence 5, Appli
c	38	38.6	1.4	1581	2	US-08-762-106-6	Sequence 6, Appli
c	39	38.6	1.4	1581	3	US-09-320-774-6	Sequence 6, Appli
	40	38.4	1.4	318	4	US-09-252-991A-10314	Sequence 10314, A
	41	38.4	1.4	387	4	US-09-252-991A-1461	Sequence 1461, Ap
	42	38.4	1.4	1272	4	US-09-252-991A-1552	Sequence 1552, Ap
c	43	38.4	1.4	2777	4	US-09-310-463-3	Sequence 3, Appli
c	44	38.4	1.4	2777	4	US-08-842-248A-3	Sequence 3, Appli
	45	38.4	1.4	50937	3	US-09-428-517-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,463
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/935,313
;       FILING DATE:
;       APPLICATION NUMBER:  EP 91 114 300.6
;       FILING DATE:  26-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703)836-9300
;       TELEFAX:  (703)683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7218 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match              2.8%;  Score 78.8;  DB 1;  Length 7218;
  Best Local Similarity   3.8%;  Pred. No. 1.7e-12;
  Matches   14;  Conservative  231;  Mismatches  123;  Indels    0;  Gaps    0;

Qy       1678 GGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGAC 1737
              | || ||  || |     ||| | ||:: :::::::: ::  ::::: :: :: :::::
Db       1460 GTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1401

Qy       1738 TTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGG 1797
                :::::  : : : ::::::  ::::   ::::: :: ::::  : :::::  : ::::
Db       1400 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1341

Qy       1798 GTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGT 1857
              :  :::: :: ::: ::::::::: : :::::: :::::::       :  :     ::
Db       1340 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1281

Qy       1858 GAACCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAA 1917
              :::  :::: ::: :::: : :::: :  ::: : :: ::: ::::::  ::  : ::::
Db       1280 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1221

Qy       1918 GAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAA 1977
              ::::::::::  ::::::: :: ::::: :::::::  :: :  ::: ::: :    :::
Db       1220 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1161

Qy       1978 CTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAG 2037
                :::::  :  :  ::::::    : :::   ::::  : :: ::: :::  ::  :::
```

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Db       1160 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1101

Qy       2038 AAGACAAA 2045
              :::: :::
Db       1100 RRRRRRRR 1093


RESULT 2
US-09-701-068-3
; Sequence 3, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
;  APPLICANT: Galil, Gad et al.
;  TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
;  TITLE OF INVENTION:  EXPRESSING SAME
;  FILE REFERENCE: 01/21317
;  CURRENT APPLICATION NUMBER: US/09/701,068
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1935
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (136)..(1755)
US-09-701-068-3

  Query Match             2.8%;  Score 76.6;  DB 4;  Length 1935;
  Best Local Similarity   51.3%;  Pred. No. 3.1e-12;
  Matches  178;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy       2174 TCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCCACAGAGT 2233
              ||  ||| || ||    | |   |||||  |||| ||||| | ||||||||||    |
Db       1169 TCTGGCATTTACTCCTCGCCCCTTGGAAACTGCTTTTTGCATTTGTGCCCCCCTGCAACA 1228

Qy       2234 ACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCA 2293
                   ||||| |||  |   |||  |  |||  ||||| ||||  |     |  ||
Db       1229 TTGCTCACGGTTGGATCGCTTTCATCTGCTCTCTCCTCTTCATCAGTGGAGTAGCCTTTG 1288

Qy       2294 TCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAG 2353
              |  |        |  |    |   | ||||   || |||  | ||    |  || | ||
Db       1289 TTGTCACAAGATTTACTGACCTTATAAGCTGTGTCACTGGAATAAACCCATATGTGATAG 1348

Qy       2354 CTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTG 2413
              |  |        | |||  ||| || ||    |||||     | || || |||   ||||
Db       1349 CATTCACAGCACTCGCAAGTGGAACTTCATGGCCAGACTTAGTAGCAAGTAAAATCGCTG 1408

Qy       2414 CCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCA 2473
              |    |   | ||   |||||  |  | ||||  ||| | ||  |||| ||| | || |
Db       1409 CAGAGCGACAACTAACCGCAGATTCAGCTATTGCAAACATCACCTGCAGTAACTCGGTGA 1468

Qy       2474 ATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
              |  |||   |||| || ||  |  | |||    |   | |  |||||
Db       1469 ACATCTATGTGGGGATTGGAGTTCCGTGGCTGATAAACACAGTCTAC 1515
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RESULT 3
US-09-701-068-1
; Sequence 1, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1950
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-701-068-1

  Query Match   2.8%; Score 76.6; DB 4; Length 1950;
  Best Local Similarity   51.3%; Pred. No. 3.2e-12;
  Matches 178; Conservative   0; Mismatches 169; Indels   0; Gaps   0;

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Qy       2174 TCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTGCCCCCCACAGAGT 2233
              ||  ||| || ||    | |   |||||  |||| ||||| | ||||||||||    |
Db       1174 TCTGGCATTTACTCCTCGCCCCTTGGAAACTGCTTTTTGCATTTGTGCCCCCCTGCAACA 1233

Qy       2234 ACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCA 2293
                   ||||| |||  |   |||  |  |||  ||||| |||| |     |  ||
Db       1234 TTGCTCACGGTTGGATCGCTTTCATCTGCTCTCTCCTCTTCATCAGTGGAGTAGCCTTTG 1293

Qy       2294 TCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAG 2353
              |  |        |  |    |   |  ||||   || |||  | ||    |  || | ||
Db       1294 TTGTCACAAGATTTACTGACCTTATAAGCTGTGTCACTGGAATAAACCCATATGTGATAG 1353

Qy       2354 CTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTG 2413
              |  |        | |||  ||| || ||    |||||     | || || |||   ||||
Db       1354 CATTCACAGCACTCGCAAGTGGAACTTCATGGCCAGACTTAGTAGCAAGTAAAATCGCTG 1413

Qy       2414 CCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCA 2473
              |    |   |  ||   |||||  |  | ||||  ||| | ||  |||| ||| | || |
Db       1414 CAGAGCGACAACTAACCGCAGATTCAGCTATTGCAAACATCACCTGCAGTAACTCGGTGA 1473

Qy       2474 ATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
              |  |||   |||| || ||  |  | |||    |   | |  |||||
Db       1474 ACATCTATGTGGGGATTGGAGTTCCGTGGCTGATAAACACAGTCTAC 1520
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RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;   APPLICANT: DORNER, F.

```
;     APPLICANT:  SCHEIFLINGER, F.
;     APPLICANT:  FALKNER, F. G.
;     TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;     NUMBER OF SEQUENCES:  52
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  1800 Diagonal Road, Suite 500
;       CITY:  Alexandria
;       STATE:  VA
;       COUNTRY:  USA
;       ZIP:  22313-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,463
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/935,313
;       FILING DATE:
;       APPLICATION NUMBER:  EP 91 114 300.6
;       FILING DATE:  26-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703)836-9300
;       TELEFAX:  (703)683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7218 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.9%;  Score 51.6;  DB 1;  Length 7218;
  Best Local Similarity   5.9%;  Pred. No. 0.00023;
  Matches   24;  Conservative  215;  Mismatches  169;  Indels    0;  Gaps    0;

Qy        395 CTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTT 454
              :: :::::  :::  ::::: :  ::::   ::::::: :::::    : ::::::::::
Db       1078 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1137

Qy        455 TAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAG 514
              :  ::    : : :  :: :   ::: :: ::  :  :::    :::::: :: :: :
Db       1138 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1197

Qy        515 GGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACG 574
                  : :  :::::  : : ::: :: :: ::  : ::: : ::: : :  ::::   :
```

```
Db       1198 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1257

Qy        575 GAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCT 634
                  ::: :    ::   : ::: :   :::::::: :: :: :: :::    : :::
Db       1258 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1317

Qy        635 TTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTT 694
              :: ::: : :::  :::: : :  ::::  :  :::::::::::  : :  :::   :::
Db       1318 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377

Qy        695 GGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAG 754
                  ::::::: ::::::::::::::::  : : : :::::::  :::   :
Db       1378 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTA 1437

Qy        755 ATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAG 802
                |||    |     |||  || ||| |||| | | ||      ||||
Db       1438 CCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAG 1485
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RESULT 5
US-09-197-649-7/c
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/C1-CON
; CURRENT APPLICATION NUMBER: US/09/197,649
; CURRENT FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: 07/829,461
; EARLIER FILING DATE: 1992-01-31
; EARLIER APPLICATION NUMBER: 07/739,055
; EARLIER FILING DATE: 1991-08-01
; EARLIER APPLICATION NUMBER: 07/561,968
; EARLIER FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match 1.8%; Score 50.2; DB 3; Length 390;
Best Local Similarity 46.0%; Pred. No. 8.4e-05;
Matches 169; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Qy       2238 CCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCAT 2297
              ||| |||   | |  | ||| ||||  | || || || | | | |  ||  || | || |
Db        375 CCATGGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT 316
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Qy       2298 TGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGT 2357
              |  | | | | |     | ||| |  |  | | |   ||   |     |||   |  ||
Db        315 CGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT 256

Qy       2358 TGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCT 2417
              ||  |||| |   | | |  |   |||   |      | | |  |   |  |  | | |
Db        255 CGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT 196

Qy       2418 CCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGT 2477
              |   |  ||    |  | || |  | | | |  |||    | |  |  || ||||   ||
Db        195 CGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT 136

Qy       2478 CTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACA 2537
              | || | | | ||| | | | |     ||| | || | ||  |   |   |    |
Db        135 CGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT 76

Qy       2538 GGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGC 2597
              |   ||  |||    | || |    | | | ||  ||||  | || ||  | || | |
Db         75 CGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT 16

Qy       2598 ATTTGTC 2604
                |  |||
Db         15 CGTCGTC 9
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RESULT 6
US-09-016-434-1199
; Sequence 1199, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```
;       NAME:  Zeller, Karen J.
;       REGISTRATION NUMBER:  37,071
;       REFERENCE/DOCKET NUMBER:  PA-0002 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 855-0555
;       TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  1199:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3984 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  GENBANK
;       CLONE:  g181907
US-09-016-434-1199

  Query Match             1.7%;  Score 46.2;  DB 4;  Length 3984;
  Best Local Similarity   51.7%;  Pred. No. 0.0065;
  Matches  105;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy       2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
              | |  |||||  | || | |  | | || ||||  | |||   |||||    |  || ||
Db        674 GCCTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGC 733

Qy       2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
              |||||  | || |   || |||   ||||   |  ||  || ||       |  | |  |
Db        734 GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 793

Qy       2554 GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
              ||  ||   ||  | |  || |  |  | |||  |||| | || |   ||| | | | |
Db        794 CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 853

Qy       2614 GTGCTCTTGTACCGAAGGCGGCC 2636
              |   |||  | | | | |   ||
Db        854 GCCGTCTCCTTCTGGAAGACACC 876


RESULT 7
US-09-919-172-61
; Sequence 61, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT:  Turner, Christopher M.
;  TITLE OF INVENTION: PROSTATE CANCER MARKERS
;  FILE REFERENCE: PA-0036 US
;  CURRENT APPLICATION NUMBER: US/09/919,172
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 60/222,469
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PERL Program
; SEQ ID NO 61
;   LENGTH: 4559
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673545 008942.10
US-09-919-172-61

  Query Match             1.7%;  Score 46.2;  DB 4;  Length 4559;
  Best Local Similarity   51.7%;  Pred. No. 0.0071;
  Matches  105;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy       2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
              | |  |||||  | || | |  | | || ||||  | |||   |||||    |  || ||
Db       1233 GCCTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGC 1292

Qy       2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
              |||||  | || |   || |||   ||||   |  ||  || ||       |  | |  |
Db       1293 GTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGG 1352

Qy       2554 GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
              ||  ||   ||  | |  || |  |  | |||  |||| | || |   ||| | | | |
Db       1353 CCCATCAAGGTGAACCTGGCCCTGCCTGTGTTCTTCATCCTGGCCTGCCTCTTCCTGATC 1412

Qy       2614 GTGCTCTTGTACCGAAGGCGGCC 2636
              |   |||  | | | | |   ||
Db       1413 GCCGTCTCCTTCTGGAAGACACC 1435


RESULT 8
US-09-701-068-4
; Sequence 4, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
;  APPLICANT: Galil, Gad et al.
;  TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
;  TITLE OF INVENTION:  EXPRESSING SAME
;  FILE REFERENCE: 01/21317
;  CURRENT APPLICATION NUMBER: US/09/701,068
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 2803
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-701-068-4

  Query Match             1.6%;  Score 44.8;  DB 4;  Length 2803;
  Best Local Similarity   52.1%;  Pred. No. 0.013;
  Matches  100;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        477 GTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTT 536
              |||   |  |   | ||| || |||   ||  |||| ||    || || ||  |  | ||
Db        950 GTTTTGTCATATAGGTCTTGGTCCTGGAACACTTGTTGGCTCAGCTGCATTTGATCTTTT 1009

Qy        537 CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596
              |  ||||   |   | ||||||   |||     ||  |||||       |||||     |
Db       1010 CCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGAGAACTGAAAAAGATATCCGA 1069
```

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Qy        597 TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656
              || | || |   |  |       |  |||  | | |  || ||||||||||| || ||
Db       1070 CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGGGCTTACATCTGGCTATACAT 1129

Qy        657 GATTCTGGCAGT 668
              || || |  ||
Db       1130 AATCCTCGAGGT 1141


RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             1.6%;  Score 44.2;  DB 3;  Length 4403765;
  Best Local Similarity   46.3%;  Pred. No. 3;
  Matches  145;  Conservative    0;  Mismatches  168;  Indels    0;  Gaps    0;

Qy       2213 CCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCA 2272
              |||   |  || ||   |    | ||  |||| | ||| ||| |||||   ||     |
Db    3929402 CCTCCCTTACCGCCGTTGCCGCCGGCGCCGGCGGCGCCGGCTACGCCGCTGCCGAATCCC
3929343

Qy       2273 TCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTG 2332
              |   | |    || ||||| ||      | |   |||| |  |  ||||  | || | |
Db    3929342 GCGCCGCCGCCTTCGCCGCCGTCCCCACCGTCACCGCCTTGGCCGCCGGCGCCGCCCTCG
3929283

Qy       2333 GTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATA 2392
              || | | |  |      | | | | |   ||    |      | ||  || | | | |
Db    3929282 CTCGCCACGCCTGTCGTTCCGTTCTGGCCGTCACCACCGGCCCCGCCGGTGCCGCCGGTG
3929223

Qy       2393 CGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACG 2452
              |    | |  |   | ||| |||  |   |  ||    || | | || || | | |  |
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Db    3929222 CCGCCGGCCCCGTTGATGCCGCCGGCGCCGGCGTTGCCGCCGGCCCCGCCTTGGCCGCCT
3929163

Qy       2453 TGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCG 2512
              || | | | || | |||||    |||||    |    || |   | |     |   ||||
Db    3929162 TGGCCGCCGGCGAAGCCGTTGCCGTCTTGGGAGAGGGCGCCGCTGTCGCCGGCCCCGCCG
3929103

Qy       2513 CCATCTACTGGGC 2525
                |  |  |  |||
Db    3929102 TCGCCGCCGCGGC 3929090
```

RESULT 10
US-09-252-991A-9693/c
; Sequence 9693, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9693
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9693

Query Match 1.6%; Score 43.8; DB 4; Length 1992;
Best Local Similarity 47.5%; Pred. No. 0.021;
Matches 162; Conservative 0; Mismatches 177; Indels 2; Gaps 1;

```
Qy       2372 TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431
              |||||||  ||   || | | ||  |||  || | |||||||||   | ||| |||   |
Db        738 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--GCCGGACGTACCAG 681

Qy       2432 CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCG 2491
              | | || |    |   |  | |  | ||   |  | ||| |   || |  |||| |  |
Db        680 CCGGCGGCCTGTTCCCCGCCTTCGCCGGGGTCGCCACCGGCCTGGTATCGCTGGCCGGCT 621

Qy       2492 GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551
                |    |  | |  |||| ||| |   | |||  | || |   | ||   | | |
Db        620 TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCCTGCGCAGCG 561

Qy       2552 CGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCA 2611
                      |  || |  |   |  |    |   |  |  ||  ||  |  ||  | |
Db        560 ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 501

Qy       2612 GCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671
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                || || || |||  ||   | | |   |||||     |   || |     | | | |||
Db        500 GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 441

Qy       2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712
              ||  | |||||||      ||||   |    ||||  ||||
Db        440 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 400


RESULT 11
US-09-252-991A-9558
; Sequence 9558, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 9558
;   LENGTH: 2658
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9558

  Query Match             1.6%;  Score 43.8;  DB 4;  Length 2658;
  Best Local Similarity   47.5%;  Pred. No. 0.026;
  Matches  162;  Conservative    0;  Mismatches  177;  Indels    2;  Gaps    1;

Qy       2372 TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431
              |||||||  ||   || | | ||  |||  || | |||||||||   | |||  |||   |
Db       1007 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--GCCGGACGTACCAG 1064

Qy       2432 CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCG 2491
              | | || |    |   | | | | ||   |  | ||| |   || |  |||| |  |
Db       1065 CCGGCGGCCTGTTCCCCGCCTTCGCCGGGGTCGCCACCGGCCTGGTATCGCTGGCCGGCT 1124

Qy       2492 GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551
               |     |  | |  |||| ||| |   | |||  | || |   | ||   | | |
Db       1125 TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCCTGCGCAGCG 1184

Qy       2552 CGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCA 2611
                    |  || |  |   |  |    |   |  |  ||  ||  |  ||  | |
Db       1185 ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 1244

Qy       2612 GCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671
              || || || |||  ||   | | |   |||||     |   || |     | | | |||
Db       1245 GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 1304

Qy       2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712
              ||  | |||||||      ||||   |    ||||  ||||
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```
Db       1305 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 1345


RESULT 12
US-09-252-991A-9604
; Sequence 9604, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 9604
;   LENGTH: 2799
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9604

  Query Match             1.6%;  Score 43.8;  DB 4;  Length 2799;
  Best Local Similarity   47.5%;  Pred. No. 0.027;
  Matches  162;  Conservative    0;  Mismatches  177;  Indels    2;  Gaps    1;

Qy       2372 TTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATG 2431
             |||||||  ||   || | | ||  |||  || | |||||||||    | ||| |||   |
Db       1285 TTGGCACAGCTCGGCCTGTTCCGCCTGCTCGCCACGCTGCTGCC--GCCGGACGTACCAG 1342

Qy       2432 CAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCG 2491
             | | || |    |   |  | |  | ||   |  | ||| |   || |  |||| |  |
Db       1343 CCGGCGGCCTGTTCCCCGCCTTCGCCGGGGTCGCCACCGGCCTGGTATCGCTGGCCGGCT 1402

Qy       2492 GCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGT 2551
              |     |  | |  |||| ||| |   | |||  | || |   | ||   | | |
Db       1403 TCGCCCTCCCGCCGCTGGCAGCCCTGGGCCGGGTACCGCCGTTGCGGGTCCTGCGCAGCG 1462

Qy       2552 CGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCA 2611
                    |  || |  |   |  |    |   |  |  ||  ||  |  ||  | |
Db       1463 ACCTGCTGCCGGTGCCGATGCGCACCTGGATGGCCTACGCCTGCGCCCTGCTCGCCCTGG 1522

Qy       2612 GCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCT 2671
             || || || |||  ||   | | |   |||||     |   || |     | | | |||
Db       1523 GCCTGATCATGTGGCGGTTGAGTCTCGACCTGAAGCTGACCCTCGCCCTGCTCGGCGGCG 1582

Qy       2672 GCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTC 2712
             ||  | |||||||      ||||   |    ||||  ||||
Db       1583 GCCTGGTCGCCACGCTGGTGCTCGGCGCCCTCCTGCTGCTC 1623


RESULT 13
US-09-103-840A-1/c
```

; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 1.6%; Score 43.4; DB 3; Length 4411529;
Best Local Similarity 47.3%; Pred. No. 5.2;
Matches 131; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

```
Qy       2241 CGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGG 2300
              ||||   ||| ||  ||||| | ||  | | | |    |      |  ||||  | | ||
Db    3932453 CGGCCCCGCCGGCCCCGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCCGTCGG
3932394

Qy       2301 GGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGT 2360
              | |    || |   | |   | |||||   |    | | |   | | | | ||  | |
Db    3932393 CGCCAATCCCGCTGGCATTATCAGCACCGGAGCCACCCATGCCGCCGGCGCCGCCTTGGC
3932334

Qy       2361 TTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCA 2420
                ||  ||    |||||| | |   | | |      ||| |||| |  | ||||  ||
Db    3932333 CGCCGGTGCCGCCGGCACCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCT
3932274

Qy       2421 GGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTT 2480
              ||  |   | || | || | ||    || |         || |         |  ||
Db    3932273 GGCCGCCGACGCCGCCGGCCCCGCCAGCGAACCCGGTACCACCGGTTAGACCTGTGCTGG
3932214

Qy       2481 CCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATC 2517
              |  |||| |||||   | | | ||||   |||||| |
Db    3932213 CGGGGGCGTCGGCGCCGGCCGCTCCGGCACCGCCAGC 3932177
```

RESULT 14
US-09-252-991A-5866
; Sequence 5866, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5866
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5866

Query Match 1.5%; Score 42.2; DB 4; Length 660;
Best Local Similarity 46.7%; Pred. No. 0.03;
Matches 134; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

```
Qy       2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
              | || | || | | ||   ||    || ||  ||||| |    || |  || ||  |
Db        302 GTCGTCGCCCTGGTCATGCTGGTCCGCGGCTTCGCCGACGCGATCATGATGCGCGGCCAA 361

Qy       2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
              ||||||  | |||  | ||||| | || |    ||||  |    || | | | ||  |
Db        362 CTGGCCCTGGCCGAAGGCGCCAACCACGGCTACCTGCCGCCGGAGCACTACGACCAGATC 421

Qy       2554 GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
                | | | |  | | |   | | | | ||||||    | |  | ||  |   |  |
Db        422 TTCACCGCGCATGGCGTGATCATGATCATCTTCATGGCCATGCCGTTCATGACCGGCCTG 481

Qy       2614 GTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGC 2673
              ||  | ||  |     || || |  |   |   | ||  | |    ||||     |  |
Db        482 ATGAACCTGGCCGTGCCGCTGCAGATCGGCGCGCGCGACGTGGCGTTCCCCTTCCTCAAC 541

Qy       2674 AAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACAT 2720
                |||   |        |||| | || |||     |||  || || |
Db        542 TCGCTGAGCTTCTGGCTGCTCGTGGTCAGCGCCATGCTGGTCAACGT 588
```

RESULT 15
US-09-252-991A-5825
; Sequence 5825, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5825
;   LENGTH: 1983
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5825

  Query Match   1.5%; Score 42.2; DB 4; Length 1983;
  Best Local Similarity   46.7%; Pred. No. 0.063;
  Matches 134; Conservative   0; Mismatches 153; Indels   0; Gaps   0;

```
Qy       2434 GACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGC 2493
              | || | || | | ||   ||    || ||  ||||| |    || |  || ||  |
Db        193 GTCGTCGCCCTGGTCATGCTGGTCCGCGGCTTCGCCGACGCGATCATGATGCGCGGCCAA 252

Qy       2494 CTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCG 2553
              ||||||  | |||  | ||||| | || |    |||| |    || | | | ||  |
Db        253 CTGGCCCTGGCCGAAGGCGCCAACCACGGCTACCTGCCGCCGGAGCACTACGACCAGATC 312

Qy       2554 GCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGC 2613
                | | | |  | | |   | | | | ||||||    | |  | ||  |   |  |
Db        313 TTCACCGCGCATGGCGTGATCATGATCATCTTCATGGCCATGCCGTTCATGACCGGCCTG 372

Qy       2614 GTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGC 2673
              ||  | ||  |     || || |  |   |   | ||  | |    ||||     |  |
Db        373 ATGAACCTGGCCGTGCCGCTGCAGATCGGCGCGCGCGACGTGGCGTTCCCCTTCCTCAAC 432

Qy       2674 AAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACAT 2720
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Db        433 TCGCTGAGCTTCTGGCTGCTCGTGGTCAGCGCCATGCTGGTCAACGT 479
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Search completed: June 25, 2004, 15:37:21
Job time : 228.931 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 07:13:27 ; Search time 1117.99 Seconds
(without alignments)
11333.972 Million cell updates/sec

Title: US-10-054-680-1
Perfect score: 2766
Sequence: 1 atggcgtggttaaggttgca.....gctacatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match	Length	DB	ID	Description
	1	2766	100.0	2766	14	US-10-054-680-1	Sequence 1, Appli
	2	2766	100.0	3812	14	US-10-054-680-5	Sequence 5, Appli
	3	2761.2	99.8	2782	9	US-09-804-474A-1	Sequence 1, Appli
	4	2733.4	98.8	2781	15	US-10-275-116-1	Sequence 1, Appli
	5	2673.2	96.6	2685	15	US-10-114-153-5	Sequence 5, Appli
	6	2657.6	96.1	2840	15	US-10-114-153-3	Sequence 3, Appli
	7	2367.2	85.6	2813	15	US-10-114-153-1	Sequence 1, Appli
	8	1786.4	64.6	2534	15	US-10-256-537-1	Sequence 1, Appli
	9	1786.4	64.6	2534	15	US-10-256-537-3	Sequence 3, Appli
	10	1784.8	64.5	126512	9	US-09-804-474A-3	Sequence 3, Appli
	11	1784.6	64.5	1863	14	US-10-054-680-3	Sequence 3, Appli
	12	1277	46.2	4282	15	US-10-281-866-1	Sequence 1, Appli
	13	1277	46.2	4282	15	US-10-281-866-3	Sequence 3, Appli
	14	1270.8	45.9	3004	16	US-10-388-934-506	Sequence 506, App
	15	1227.8	44.4	4087	9	US-09-901-419-1	Sequence 1, Appli
	16	1207.2	43.6	6106	16	US-10-062-674-1648	Sequence 1648, Ap
	17	897.4	32.4	1187	13	US-10-243-552-809	Sequence 809, App
	18	821.4	29.7	823	15	US-10-029-386-20265	Sequence 20265, A
	19	787.2	28.5	1836	9	US-09-864-761-16939	Sequence 16939, A
	20	503.4	18.2	505	15	US-10-029-386-6536	Sequence 6536, Ap
	21	494	17.9	551	15	US-10-029-386-4103	Sequence 4103, Ap
	22	366	13.2	366	15	US-10-029-386-17804	Sequence 17804, A
	23	336.4	12.2	507	15	US-10-029-386-4003	Sequence 4003, Ap
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	26	208.4	7.5	280	15	US-10-029-386-21161	Sequence 21161, A
	27	186.4	6.7	491	9	US-09-864-761-646	Sequence 646, App
	28	186.2	6.7	276	9	US-09-864-761-17437	Sequence 17437, A
	29	180	6.5	180	15	US-10-029-386-17706	Sequence 17706, A
	30	169	6.1	477	10	US-09-918-995-2005	Sequence 2005, Ap
	31	164.2	5.9	459	9	US-09-864-761-102	Sequence 102, App
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	33	108	3.9	1302	13	US-10-243-552-276	Sequence 276, App
c	34	95	3.4	151	9	US-09-864-761-17938	Sequence 17938, A
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	38	73.4	2.7	968	13	US-10-424-599-94222	Sequence 94222, A
	39	60	2.2	128	9	US-09-864-761-20736	Sequence 20736, A
c	40	60	2.2	136	15	US-10-029-386-23072	Sequence 23072, A
	41	60	2.2	467	9	US-09-864-761-3975	Sequence 3975, Ap
c	42	60	2.2	546	13	US-10-027-632-247268	Sequence 247268,
c	43	60	2.2	546	16	US-10-027-632-247268	Sequence 247268,
c	44	60	2.2	599	15	US-10-029-386-9372	Sequence 9372, Ap
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ALIGNMENTS

RESULT 1
US-10-054-680-1
; Sequence 1, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998Alel Human Ion Exchanger Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2766
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-1

Query Match 100.0%; Score 2766; DB 14; Length 2766;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
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Db       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100

Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
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Qy        2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
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Qy        2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
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Qy        2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Db        2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520

Qy        2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
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Qy        2761 TTCTAA 2766
                ||||||
Db        2761 TTCTAA 2766
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RESULT 2
US-10-054-680-5
; Sequence 5, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5
; LENGTH: 3812
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-5

Query Match 100.0%; Score 2766; DB 14; Length 3812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       1458 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1518 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       1578 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1698 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1938 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       2118 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2177
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       2178 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2238 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2297

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
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Db       2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 2417

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
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Db       2418 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 2477

Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
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Db       2478 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 2537

Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2538 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 2597

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
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Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
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Db       2658 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2717

Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
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Db       2718 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2777

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
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Db       2778 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2837

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2838 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2897

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2898 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2957

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2958 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 3017

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
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Db       3018 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 3077

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
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Db       3078 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 3137

Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3138 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 3197

Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3198 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 3257

Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
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Db       3258 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 3317

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
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Db       3318 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 3377

Qy       2761 TTCTAA 2766
                ||||||
Db       3378 TTCTAA 3383
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RESULT 3
US-09-804-474A-1
; Sequence 1, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
; APPLICANT: KODET, Stefan et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000891
; CURRENT APPLICATION NUMBER: US/09/804,474A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Human
US-09-804-474A-1

Query Match 99.8%; Score 2761.2; DB 9; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69
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Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db       130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

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Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db       310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db       370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729

Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789

Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db      1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089

Qy      1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy      1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db      1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209

Qy      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db      1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy      1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db      1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1809

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1869

Qy       1861 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 CCGAAATGGATGGAACGTGGAATATCAGATGTGACAGACAGGAAGCTGACTATGGAAGAA 1929

Qy       1921 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 GAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAACACCCCAAACTG 1989

Qy       1981 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1990 GAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTGGACAAACTGATCAAGAAG 2049

Qy       2041 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2050 ACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTCATGGAGGCCATC 2109

Qy       2101 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 ACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGGGAGGAGAGGCTGCCCTCC 2169

Qy       2161 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 TGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAGGTGCTGTTTGCCTGTGTG 2229

Qy       2221 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 CCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTCTCCATCCTCATCATTGGC 2289

Qy       2281 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 ATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGCTGCACCATTGGTCTCAAA 2349

Qy       2341 GATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2400
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GATTCGGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCTGTCCCAGATACGTTTGCC 2409

Qy       2401 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCCATTGGCAACGTGACGGGC 2469

Qy       2461 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 AGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTAC 2529

Qy       2521 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 TGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACC 2589

Qy       2581 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 CTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCAC 2649
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Qy       2641 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 CTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTG 2709

Qy       2701 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 AGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGG 2769

Qy       2761 TTCTAA 2766
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Db       2770 TTCTAA 2775
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RESULT 4
US-10-275-116-1
; Sequence 1, Application US/10275116
; Publication No. US20030096312A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein
; FILE REFERENCE: HNCX3CWWS
; CURRENT APPLICATION NUMBER: US/10/275,116
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2781)
US-10-275-116-1

4/30/01

Query Match 98.8%; Score 2733.4; DB 15; Length 2781;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAAACCATAAGGGTT 1800

Qy       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGAATTTCTTCATTGCCCTTGGTGAA 1860

Qy       1861 CCGAAATGGATGGAACGTGGAATATC----------------AGATGTGACAGACAGG 1902
             |||||||||||||||||||||||||                |||||||||||||||
Db       1861 CCGAAATGGATGGAACGTGGAATATCAGGTGTGAGATTCTTTAAAGATGTGACAGACAGG 1920

Qy       1903 AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG 1962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTG 1980
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Qy       1963 GGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG 2022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GGTGAACACCCCAAACTAGAAGTCATCATTGAAGAGTCCTATGAGTTCAAGACTACGGTG 2040

Qy       2023 GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGAC 2082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GACAAACTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGAC 2100

Qy       2083 CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG 2142
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Db       2101 CAGTTCATGGAGGCCATCACCGTCAGTGCAGCAGGGGATGAGGATGAGGATGAATCCGGG 2160

Qy       2143 GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG 2202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTCTGGAAG 2220

Qy       2203 GTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC 2262
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Db       2221 GTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTCGCCGTC 2280

Qy       2263 TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC 2322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTCGGC 2340

Qy       2323 TGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCT 2382
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Db       2341 TGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACCTCT 2400

Qy       2383 GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC 2442
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Db       2401 GTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCCTCC 2460

Qy       2443 ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG 2502
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Db       2461 ATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCCTGG 2520

Qy       2503 TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA 2562
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Db       2521 TCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGCACA 2580

Qy       2563 CTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG 2622
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Db       2581 CTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTCTTG 2640

Qy       2623 TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC 2682
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Db       2641 TACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCC 2700

Qy       2683 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2742
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Db       2701 ACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCC 2760

Qy       2743 TATTGCTACATCAAGGGGTTC 2763
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Db       2761 TATTGCTACATCAAGGGGTTC 2781
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RESULT 5
US-10-114-153-5
; Sequence 5, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13

4/1/04

; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 5
;   LENGTH: 2685
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2685)
US-10-114-153-5

  Query Match   96.6%; Score 2673.2; DB 15; Length 2685;
  Best Local Similarity 99.9%; Pred. No. 0;
  Matches 2675; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy         86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 145
              ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 61

Qy        146 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 205
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Db         62 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 121

Qy        206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
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Db        122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy        266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
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Db        182 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 241

Qy        326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 385
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Qy        386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 445
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Qy        506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 565
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Qy        566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
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Db        482 TCCCAGACGGAGAGACTCGCAAGATCAAACATCTACGAGTCTTCTTCATCACCGCTGCTT 541

Qy        626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
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Qy       686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745
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Qy       806 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 865
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Db       722 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 781

Qy       866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 925
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Db       782 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 841

Qy       926 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 985
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       842 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 901

Qy       986 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 1045
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Db       902 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 961

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Db       962 AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1021

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Qy      1166 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1225
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Qy      1226 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1285
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Db      1142 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1201

Qy      1286 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1345
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Db      1322 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1381

Qy      1466 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1525
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Db      1382 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1441

Qy      1526 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1585
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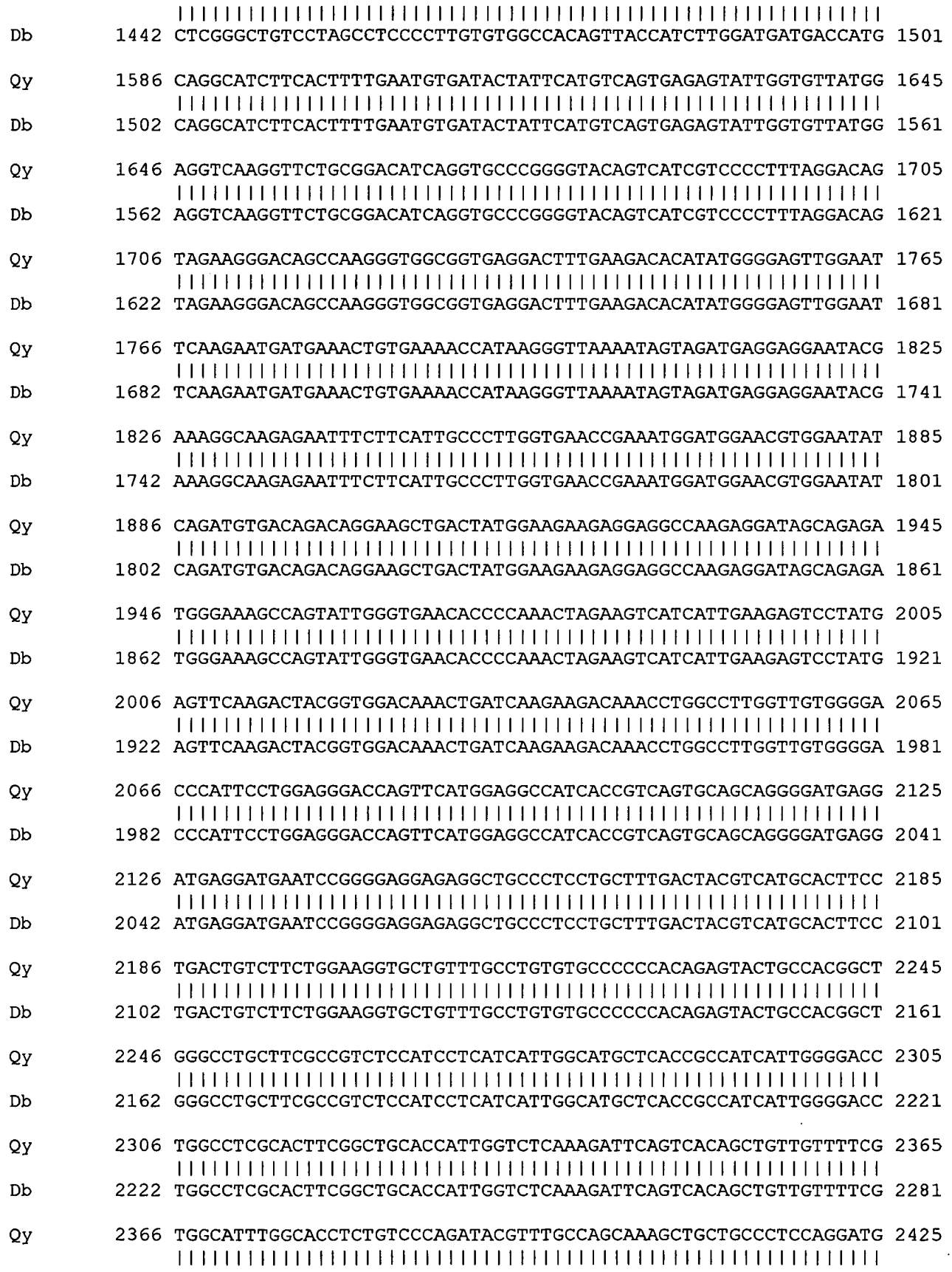

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Db       2342 TATATGCAGACGCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGG 2401

Qy       2486 GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC 2545
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Db       2402 GCATCGGCCTGGCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCC 2461

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Db       2462 ACGTGTCGGCCGGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCT 2521

Qy       2606 GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC 2665
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Db       2522 GCATCAGCGTGCTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCC 2581

Qy       2666 GTGGCTGCAAGCTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCT 2725
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Qy       2726 TTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC 2763
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RESULT 6
US-10-114-153-3
; Sequence 3, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John

; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 3
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2838)
US-10-114-153-3

Query Match 96.1%; Score 2657.6; DB 15; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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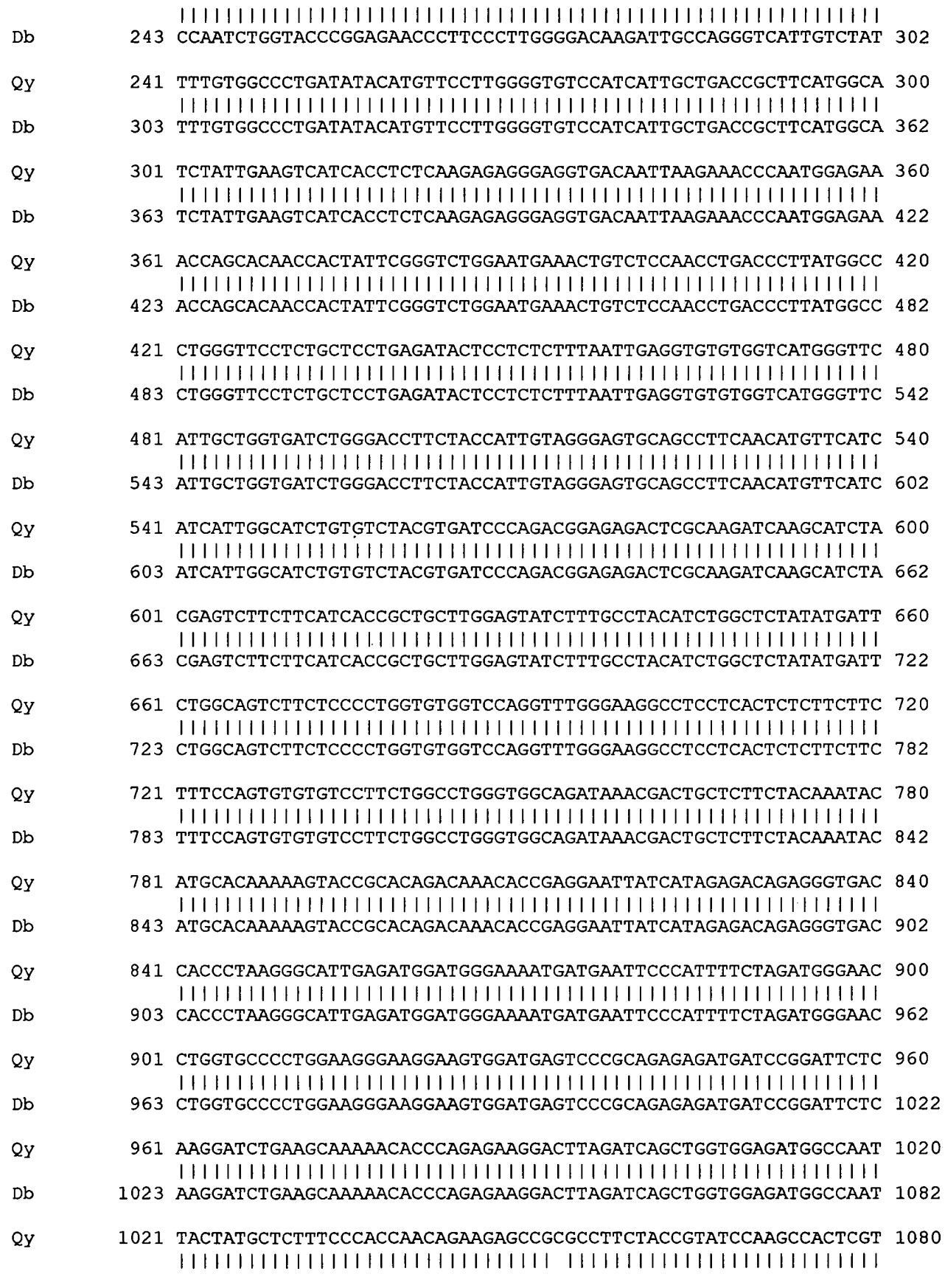

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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1909 ACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGGTGAA 1968
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Qy       2029 CTGATCAAGAAGACAAACCTGGCCTTGGTTGTGGGGACCCATTCCTGGAGGGACCAGTTC 2088
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Qy       2749 TACATCAAGGGGTTCTAA 2766
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Db       2823 TACATCAAGGGGTTCTAA 2840
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RESULT 7
US-10-114-153-1
; Sequence 1, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657

; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 1
;   LENGTH: 2813
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9)..(2793)
US-10-114-153-1

  Query Match   85.6%; Score 2367.2; DB 15; Length 2813;
  Best Local Similarity   91.2%; Pred. No. 0;
  Matches 2542; Conservative   0; Mismatches 223; Indels   21; Gaps   2;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          9 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 68

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         69 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        249 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        429 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 488

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        489 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 548
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        549 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 608

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        609 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 668

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        669 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 728

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db        729 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 788

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db        789 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 848

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db        849 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 908

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db        909 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 968

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db        969 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1028

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1029 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1088

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1089 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1148

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1149 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1208

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1209 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1268

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       1269 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1328

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1329 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1388
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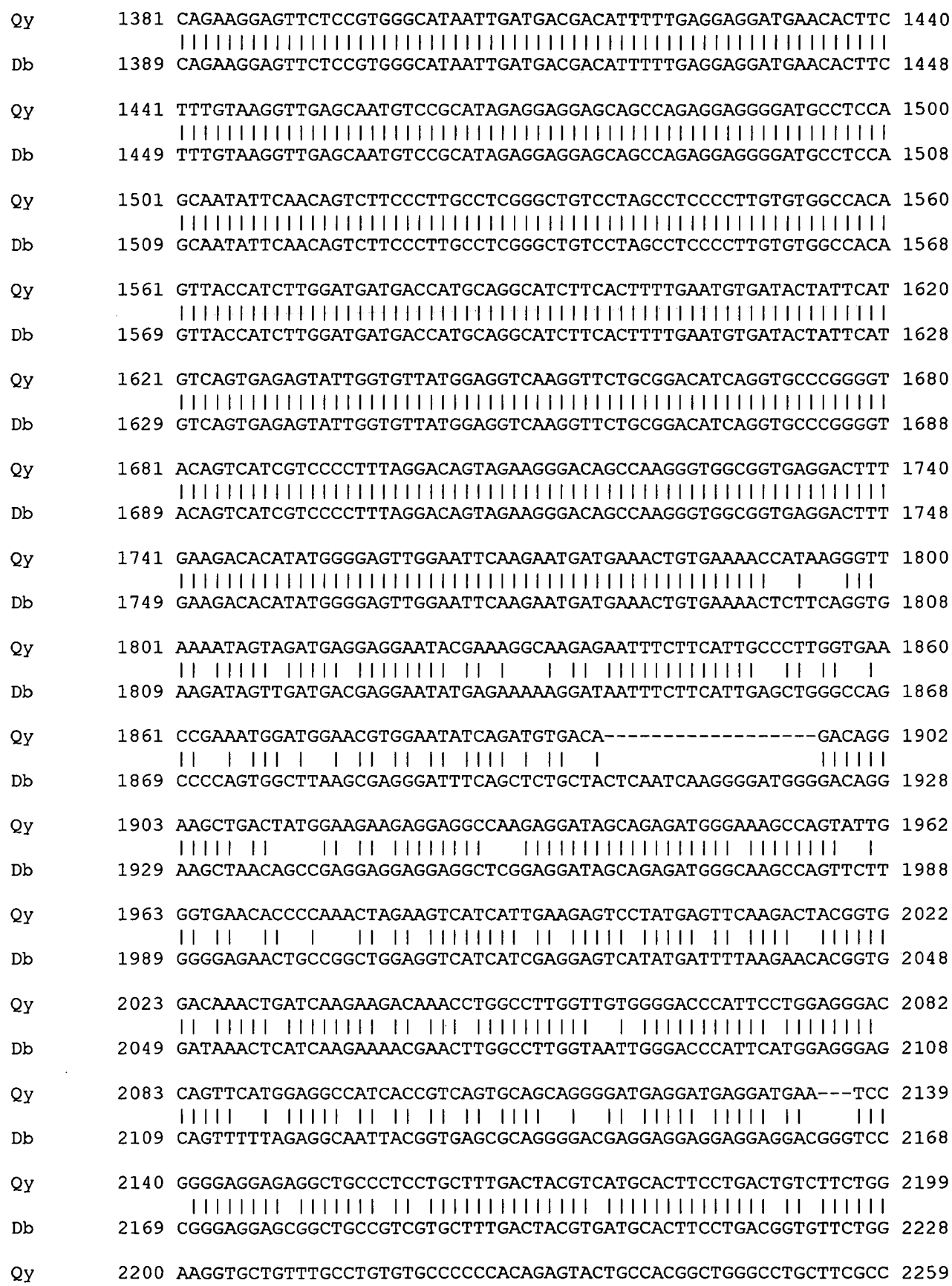

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Qy        2260 GTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCACTTC 2319
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Db        2289 GTCTCCATCCTGGTCATCGGCCTGCTCACCGCCCTCATTGGGGACCTCGCCTCCCACTTC 2348

Qy        2320 GGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGCACC 2379
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Db        2349 GGCTGCACCGTTGGCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGCACC 2408

Qy        2380 TCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGACGCC 2439
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Db        2409 TCCATCCCTGACACGTTCGCCAGCAAGGTGGCGGCGCTGCAGGACCAGTGCGCCGACGCG 2468

Qy        2440 TCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTGGCC 2499
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Db        2469 TCCATCGGCAACGTGACCGGCTCCAACGCGGTGAACGTGTTCCTTGGCCTGGGCGTCGCC 2528

Qy        2500 TGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCCGGC 2559
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Db        2529 TGGTCTGTGGCCGCCGTGTACTGGGCGGTGCAGGGCCGCCCCTTCGAGGTGCGCACTGGC 2588

Qy        2560 ACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTGCTC 2619
               ||  ||||||||||||||||  |||||||||  ||||  ||  ||  ||  ||||    ||||||
Db        2589 ACGCTGGCCTTCTCCGTCACGCTCTTCACCGTCTTCGCCTTCGTGGGCATTGCCGTGCTG 2648

Qy        2620 TTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAGCTC 2679
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Db        2649 CTGTACCGGCGCCGGCCGCACATCGGCGGCGAGCTGGGCGGCCCGCGCGGACCCAAGCTC 2708

Qy        2680 GCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTAGAG 2739
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Db        2709 GCCACCACCGCGCTCTTCCTGGGCCTCTGGCTCCTGTACATCCTCTTCGCCAGCCTGGAG 2768

Qy        2740 GCCTATTGCTACATCAAGGGGTTCTA 2765
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Db        2769 GCGTACTGCCACATCCGGGGCTTCTA 2794


RESULT 8
US-10-256-537-1
; Sequence 1, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Joseph M.
;  TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
;  TITLE OF INVENTION:  NA/CA EXCHANGER FAMILY MEMBER
;  FILE REFERENCE: MPI01-231P1RM
;  CURRENT APPLICATION NUMBER: US/10/256,537
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,737
;  PRIOR FILING DATE: 2001-09-28
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2534
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-256-537-1

Query Match 64.6%; Score 1786.4; DB 15; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy         781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db        1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

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Db        1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

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Db        1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

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Db        1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy        1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db        1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy        1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy        1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db        1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy        1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db        1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy        1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy        1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

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RESULT 9
US-10-256-537-3
; Sequence 3, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Joseph M.
;  TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
;  TITLE OF INVENTION:  NA/CA EXCHANGER FAMILY MEMBER
;  FILE REFERENCE: MPI01-231P1RM
;  CURRENT APPLICATION NUMBER: US/10/256,537
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,737
;  PRIOR FILING DATE: 2001-09-28
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (343)...(2130)
US-10-256-537-3

  Query Match             64.6%;  Score 1786.4;  DB 15;  Length 2534;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1787;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788
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Db       2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGTAA 2130
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RESULT 10
US-09-804-474A-3
; Sequence 3, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
; APPLICANT: KODET, Stefan et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

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;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000891
;  CURRENT APPLICATION NUMBER: US/09/804,474A
;  CURRENT FILING DATE:  2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 126512
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(126512)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-474A-3

  Query Match             64.5%;  Score 1784.8;  DB 9;  Length 126512;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1786;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2070 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 2189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 2309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 2369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2370 ACCAGCACAACAACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 2489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 2549
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 2609

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 2669

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       2670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 2729

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       2730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 2789

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 2849

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       2850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 2909

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       2910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 2969

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       2970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 3029

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       3030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 3089

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 3149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       3150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 3209

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       3210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 3269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 3329

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       3330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 3389
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db       3390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 3449

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       3450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 3509

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       3510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 3569

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       3570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       3630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 3689

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGAAA 1788
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Db       3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGTAA 3797
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RESULT 11
US-10-054-680-3
; Sequence 3, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
;  APPLICANT: Friddle, Carl Johan
;  APPLICANT:  Hilbun, Erin
;  TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0301-USA
;  CURRENT APPLICATION NUMBER: US/10/054,680
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: US 60/263,384
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1863
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-054-680-3

  Query Match             64.5%;  Score 1784.6;  DB 14;  Length 1863;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1813;  Conservative    0;  Mismatches   24;  Indels    4;  Gaps    1;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
```

```
Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796
              ||||||||||||||||||||||||||||||||||||||||    ||||| |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800

Qy       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
              | | |  || | ||| |||||||   |    |    |||||
Db       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841


RESULT 12
US-10-281-866-1
; Sequence 1, Application US/10281866
; Publication No. US20030091570A1
; GENERAL INFORMATION:
;  APPLICANT: Silos-Santiago, Inmaculada
;  TITLE OF INVENTION: Methods and compositions for the
;  TITLE OF INVENTION:  treatment and diagnosis of pain disorders using 46556
;  FILE REFERENCE: MPI01-272P1RM
;  CURRENT APPLICATION NUMBER: US/10/281,866
;  CURRENT FILING DATE:  2002-10-28
;  PRIOR APPLICATION NUMBER: 60/335,078
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 4282
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-281-866-1

  Query Match             46.2%;  Score 1277;  DB 15;  Length 4282;
  Best Local Similarity   69.1%;  Pred. No. 0;
  Matches 1843;  Conservative    0;  Mismatches  775;  Indels   51;  Gaps    5;

Qy        130 AACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGG 189
              | ||  | |  |||    |||||  |    |||| ||  ||| ||  | |||||  | |||
Db        208 AGCACAGGGGGCTGCCAGGGGTCCTACCGCTGCCAGCCGGGGGTGCTGCTGCCCGTGTGG 267

Qy        190 TACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCC 249
               | ||  ||  |||| || || || ||||||   ||  |||   | || || |||||||||
Db        268 GAGCCCGACGACCCGTCGCTGGGTGACAAGGCGGCACGGGCAGTGGTGTACTTTGTGGCC 327

Qy        250 CTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAA 309
              || | ||||||||  || || ||||||||||  || |||||  ||||||||  | || ||
Db        328 ATGGTCTACATGTTTCTGGGAGTGTCCATCATCGCCGACCGTTTCATGGCGGCCATCGAG 387

Qy        310 GTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACA 369
              ||||||||  ||  |||||| |||| | || || |  ||  |||| || || ||||||
Db        388 GTCATCACGTCAAAAGAGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTG 447

Qy        370 ACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCC 429
               |||  ||||  |||||||||| || || |||||||| || || |||||||||| |||
Db        448 GGCACCGTTCGCATCTGGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCC 507

Qy        430 TCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGT 489
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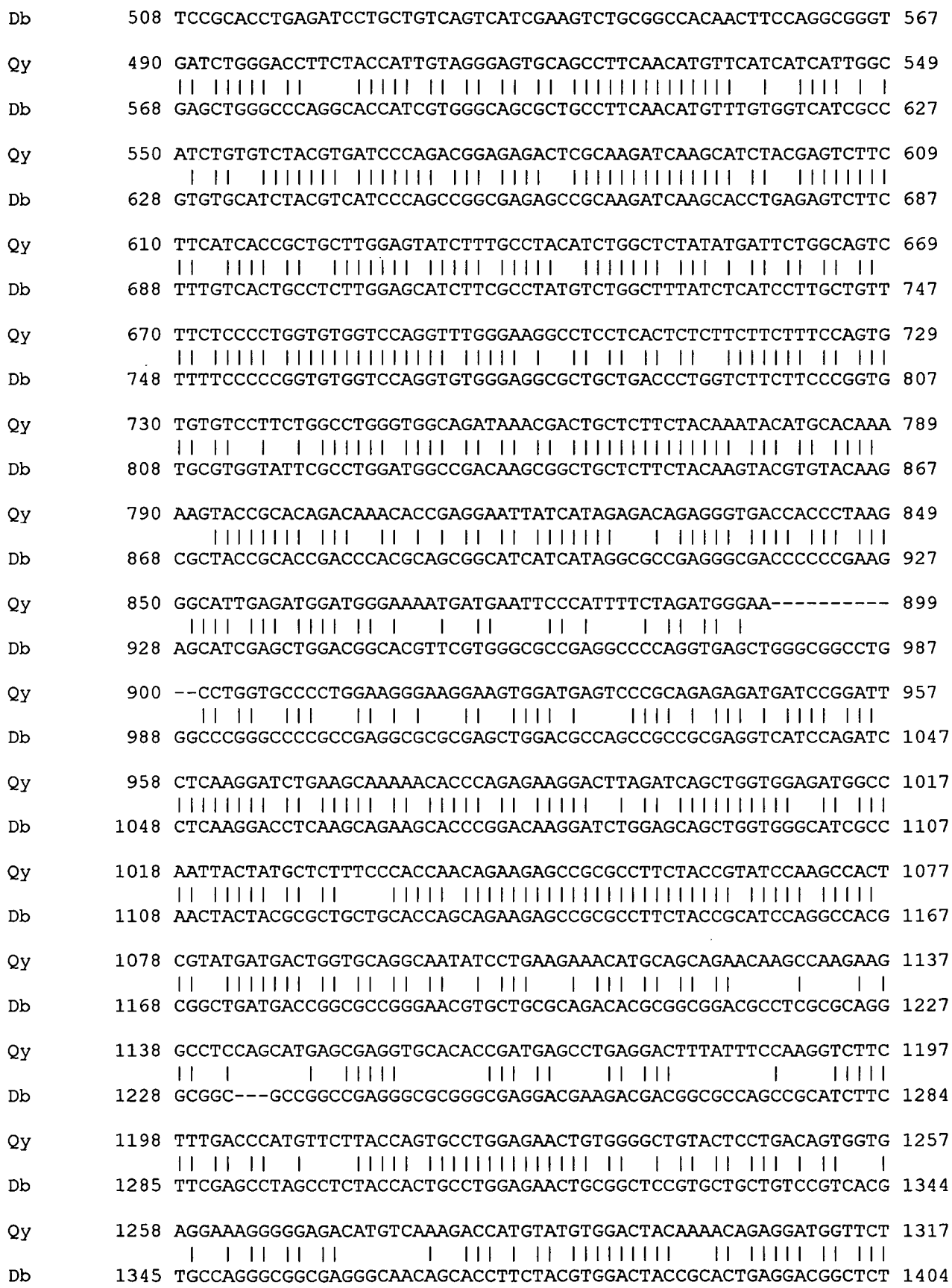

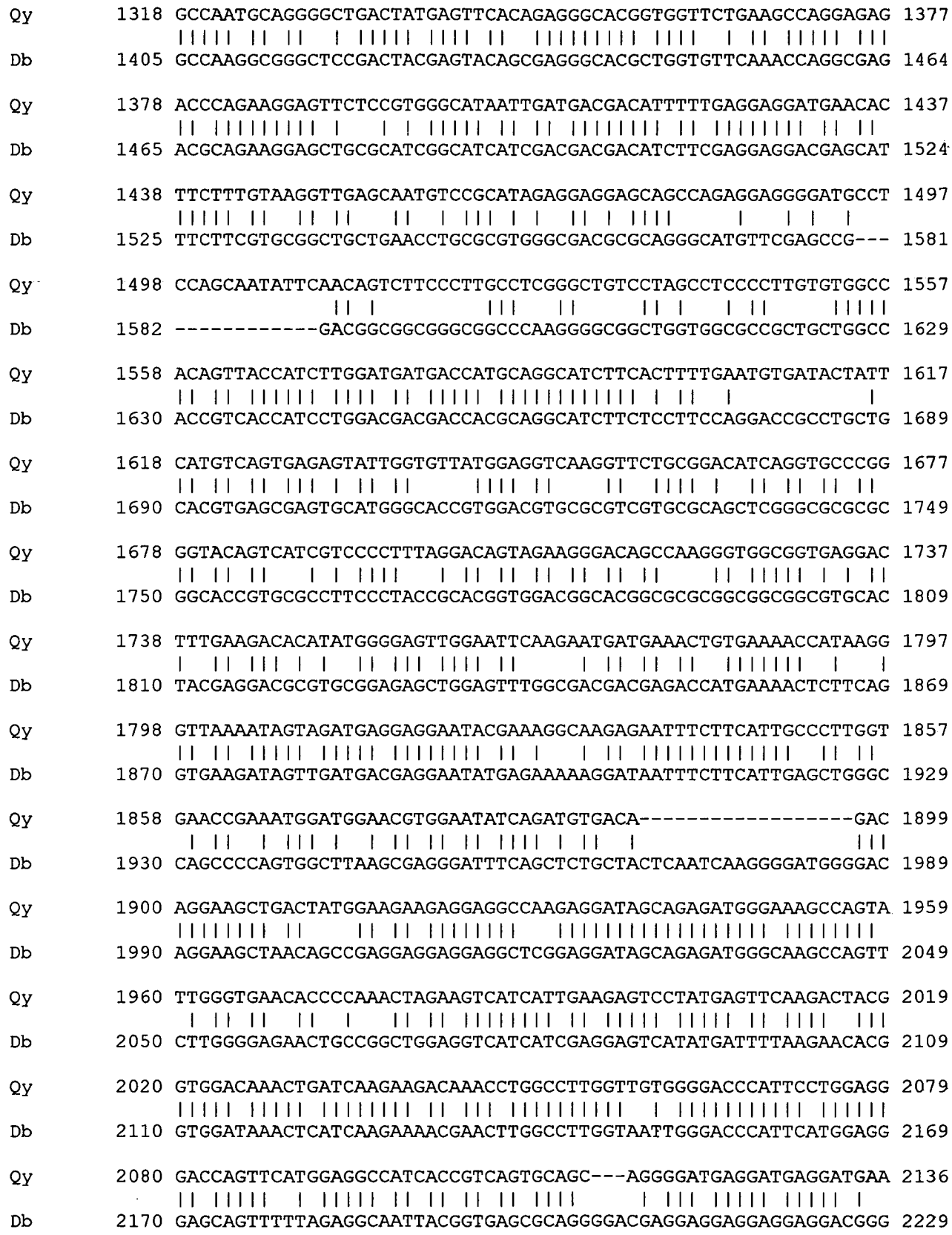

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Qy       2137 TCCGGGGAGGAGAGGCTGCCCTCCTGCTTTGACTACGTCATGCACTTCCTGACTGTCTTC 2196
Db       2230 TCCCGGGAGGAGCGGCTGCCGTCGTGCTTTGACTACGTGATGCACTTCCTGACGGTGTTC 2289

Qy       2197 TGGAAGGTGCTGTTTGCCTGTGTGCCCCCCACAGAGTACTGCCACGGCTGGGCCTGCTTC 2256
Db       2290 TGGAAGGTGCTCTTCGCCTGTGTGCCCCCCACCGAGTACTGCCACGGCTGGGCCTGCTTT 2349

Qy       2257 GCCGTCTCCATCCTCATCATTGGCATGCTCACCGCCATCATTGGGGACCTGGCCTCGCAC 2316
Db       2350 GGTGTCTCCATCCTGGTCATCGGCCTGCTCACCGCCCTCATTGGGGACCTCGCCTCCCAC 2409

Qy       2317 TTCGGCTGCACCATTGGTCTCAAAGATTCAGTCACAGCTGTTGTTTTCGTGGCATTTGGC 2376
Db       2410 TTCGGCTGCACCGTTGGCCTCAAGGACTCTGTCAATGCTGTTGTCTTCGTTGCCCTGGGC 2469

Qy       2377 ACCTCTGTCCCAGATACGTTTGCCAGCAAAGCTGCTGCCCTCCAGGATGTATATGCAGAC 2436
Db       2470 ACCTCCATCCCTGACACGTTCGCCAGCAAGGTGGCGGCGCTGCAGGACCAGTGCGCCGAC 2529

Qy       2437 GCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTG 2496
Db       2530 GCGTCCATCGGCAACGTGACCGGCTCCAACGCGGTGAACGTGTTCCTTGGCCTGGGCGTC 2589

Qy       2497 GCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCC 2556
Db       2590 GCCTGGTCTGTGGCCGCCGTGTACTGGGCGGTGCAGGGCCGCCCCTTCGAGGTGCGCACT 2649

Qy       2557 GGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTG 2616
Db       2650 GGCACGCTGGCCTTCTCCGTCACGCTCTTCACCGTCTTCGCCTTCGTGGGCATTGCCGTG 2709

Qy       2617 CTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAG 2676
Db       2710 CTGCTGTACCGGCGCCGGCCGCACATCGGCGGCGAGCTGGGCGGCCCGCGCGGACCCAAG 2769

Qy       2677 CTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTA 2736
Db       2770 CTCGCCACCACCGCGCTCTTCCTGGGCCTCTGGCTCCTGTACATCCTCTTCGCCAGCCTG 2829

Qy       2737 GAGGCCTATTGCTACATCAAGGGGTTCTA 2765
Db       2830 GAGGCGTACTGCCACATCCGGGGCTTCTA 2858
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RESULT 13
US-10-281-866-3
; Sequence 3, Application US/10281866
; Publication No. US20030091570A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MPI01-272P1RM
; CURRENT APPLICATION NUMBER: US/10/281,866
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078

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;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 4282
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (94)...(2859)
US-10-281-866-3

  Query Match           46.2%;  Score 1277;  DB 15;  Length 4282;
  Best Local Similarity  69.1%;  Pred. No. 0;
  Matches 1843;  Conservative    0;  Mismatches  775;  Indels   51;  Gaps    5;

Qy        130 AACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGG 189
              | ||  | |  |||    |||||  |    ||||  ||  |||  ||  | |||||  | |||
Db        208 AGCACAGGGGGCTGCCAGGGGTCCTACCGCTGCCAGCCGGGGGTGCTGCTGCCCGTGTGG 267

Qy        190 TACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCC 249
              | ||  ||  |||| ||  ||  ||  ||||||   ||  |||   | ||  ||  |||||||||
Db        268 GAGCCCGACGACCCGTCGCTGGGTGACAAGGCGGCACGGGCAGTGGTGTACTTTGTGGCC 327

Qy        250 CTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAA 309
              ||  | ||||||||  ||  ||  ||||||||||  ||  |||||  ||||||||  |  ||  ||
Db        328 ATGGTCTACATGTTTCTGGGAGTGTCCATCATCGCCGACCGTTTCATGGCGGCCATCGAG 387

Qy        310 GTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACA 369
              ||||||||  ||  ||||||  ||||  |  ||  ||  |  ||  ||||  ||  ||  ||||||
Db        388 GTCATCACGTCAAAAGAGAAGGAGATCACCATCACCAAGGCCAACGGTGAGACCAGCGTG 447

Qy        370 ACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCC 429
                |||  ||||  ||||||||||  ||  ||  ||||||||  ||  ||  ||||||||||  |||
Db        448 GGCACCGTTCGCATCTGGAATGAGACGGTGTCCAACCTCACGCTCATGGCCCTGGGCTCC 507

Qy        430 TCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGT 489
              ||  ||  ||||||||  ||  ||  ||  |  ||  ||  ||  ||  ||  ||  |||  ||  |||
Db        508 TCCGCACCTGAGATCCTGCTGTCAGTCATCGAAGTCTGCGGCCACAACTTCCAGGCGGGT 567

Qy        490 GATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGC 549
              ||  |||||  ||  |||||  ||  ||  ||  ||  ||||||||||||||  |  ||||  |  |
Db        568 GAGCTGGGCCCAGGCACCATCGTGGGCAGCGCTGCCTTCAACATGTTTGTGGTCATCGCC 627

Qy        550 ATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTC 609
              |  ||  |||||||  |||||||  |||  ||||  ||||||||||||||  ||  ||||||||
Db        628 GTGTGCATCTACGTCATCCCAGCCGGCGAGAGCCGCAAGATCAAGCACCTGAGAGTCTTC 687

Qy        610 TTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTC 669
              ||  ||||  ||  |||||||  |||||  |||||  |||||||  |||  |  ||  ||  ||  ||
Db        688 TTTGTCACTGCCTCTTGGAGCATCTTCGCCTATGTCTGGCTTTATCTCATCCTTGCTGTT 747

Qy        670 TTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTG 729
              ||  |||||  ||||||||||||||  |||||  |  ||  ||  ||  ||  |||||||  ||  |||
Db        748 TTTTCCCCCGGTGTGGTCCAGGTGTGGGAGGCGCTGCTGACCCTGGTCTTCTTCCCGGTG 807

Qy        730 TGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAA 789
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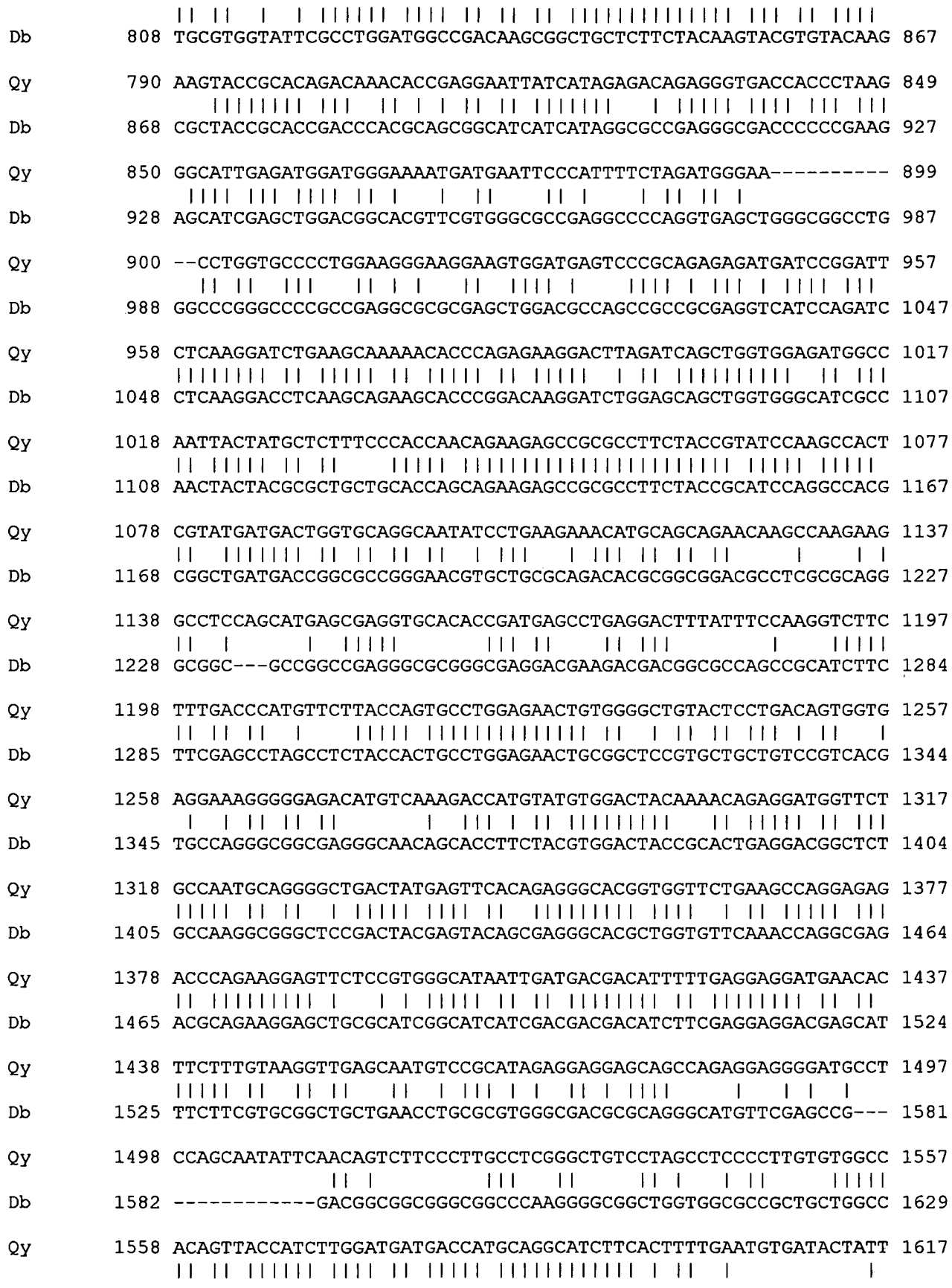

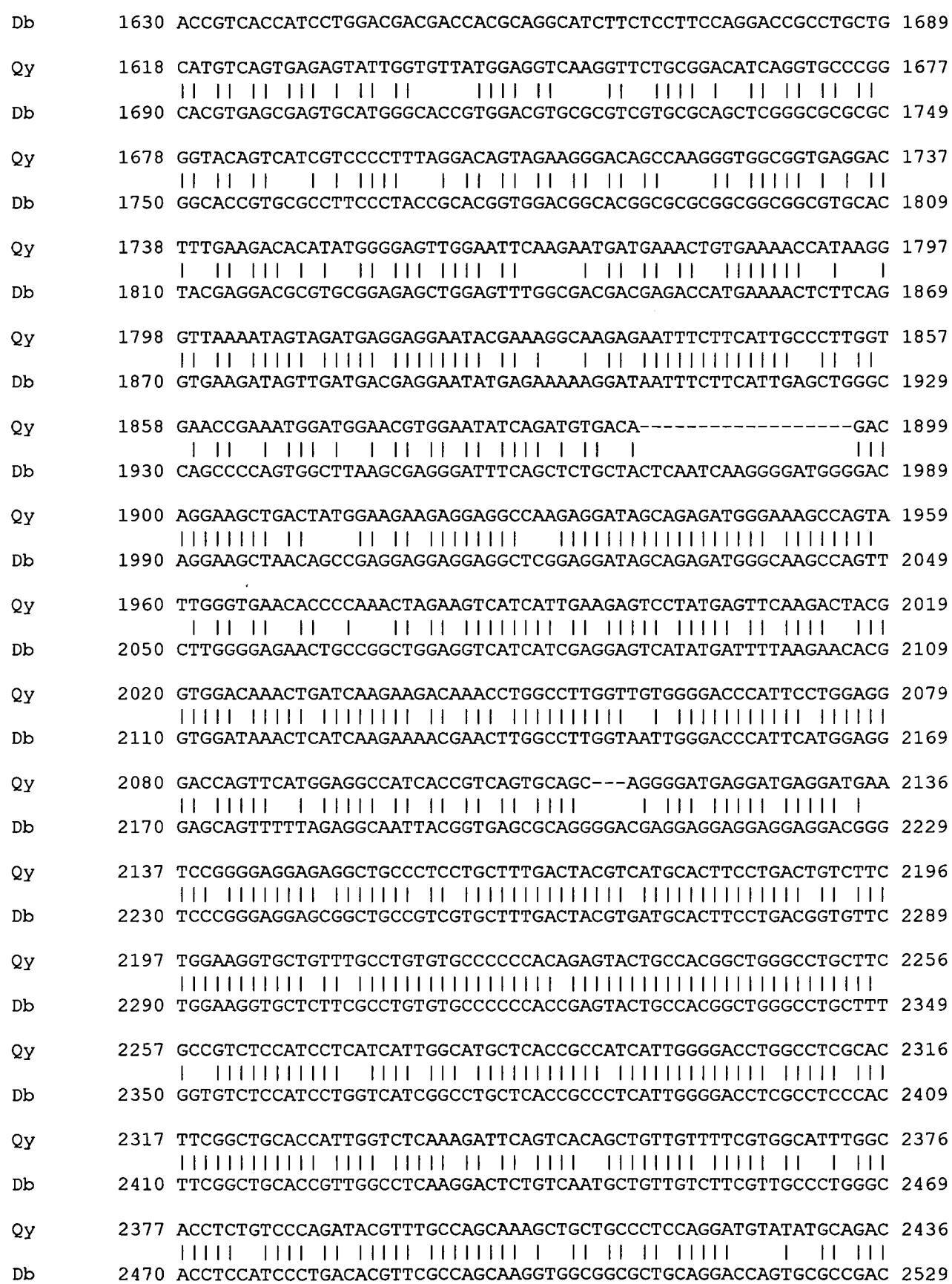

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Qy       2437 GCCTCCATTGGCAACGTGACGGGCAGCAACGCCGTCAATGTCTTCCTGGGCATCGGCCTG 2496
              || ||||| |||||||||||| |||  |||||| || || || ||||| ||| | ||| |
Db       2530 GCGTCCATCGGCAACGTGACCGGCTCCAACGCGGTGAACGTGTTCCTTGGCCTGGGCGTC 2589

Qy       2497 GCCTGGTCCGTGGCCGCCATCTACTGGGCTCTGCAGGGACAGGAGTTCCACGTGTCGGCC 2556
              |||||||| |||||||| | ||||||||  |||||||  |     ||| | |||    |
Db       2590 GCCTGGTCTGTGGCCGCCGTGTACTGGGCGGTGCAGGGCCGCCCCTTCGAGGTGCGCACT 2649

Qy       2557 GGCACACTGGCCTTCTCCGTCACCCTCTTCACCATCTTTGCATTTGTCTGCATCAGCGTG 2616
              ||||| |||||||||||||||| |||||||| |||| || || ||  ||||   ||||
Db       2650 GGCACGCTGGCCTTCTCCGTCACGCTCTTCACCGTCTTCGCCTTCGTGGGCATTGCCGTG 2709

Qy       2617 CTCTTGTACCGAAGGCGGCCGCACCTGGGAGGGGAGCTTGGTGGCCCCCGTGGCTGCAAG 2676
              ||  |||||||  | ||||||||| | || || ||||| || ||||| || ||   ||||
Db       2710 CTGCTGTACCGGCGCCGGCCGCACATCGGCGGCGAGCTGGGCGGCCCGCGCGGACCCAAG 2769

Qy       2677 CTCGCCACAACATGGCTCTTTGTGAGCCTGTGGCTCCTCTACATACTCTTTGCCACACTA 2736
              |||||||| ||   ||||||  || |||| |||||||| ||||| ||||| ||||  ||
Db       2770 CTCGCCACCACCGCGCTCTTCCTGGGCCTCTGGCTCCTGTACATCCTCTTCGCCAGCCTG 2829

Qy       2737 GAGGCCTATTGCTACATCAAGGGGTTCTA 2765
              ||||| || ||| |||||  ||| |||||
Db       2830 GAGGCGTACTGCCACATCCGGGGCTTCTA 2858
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RESULT 14
US-10-388-934-506
; Sequence 506, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 506
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
US-10-388-934-506

Query Match 45.9%; Score 1270.8; DB 16; Length 3004;
Best Local Similarity 69.0%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches 772; Indels 51; Gaps 5;

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Qy        141 CTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAA 200
              |||   ||| || |    |||| |    || ||  | |||||  | ||| | || ||  |
Db        126 CTGCCAAGGTTCCTACCGCTGCCAACCAGGGGTGCTGCTGCCTGTGTGGGAACCCGACGA 185
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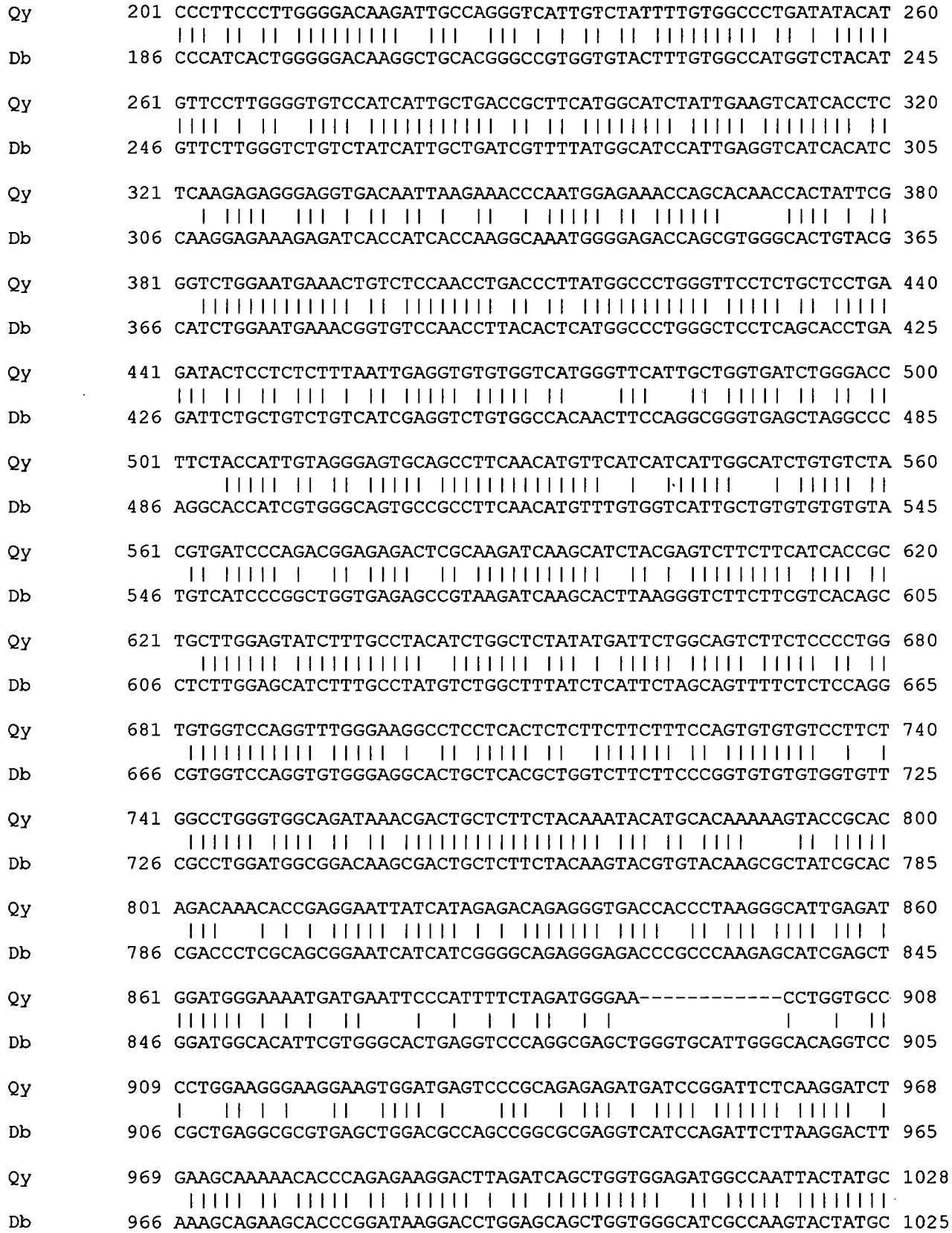

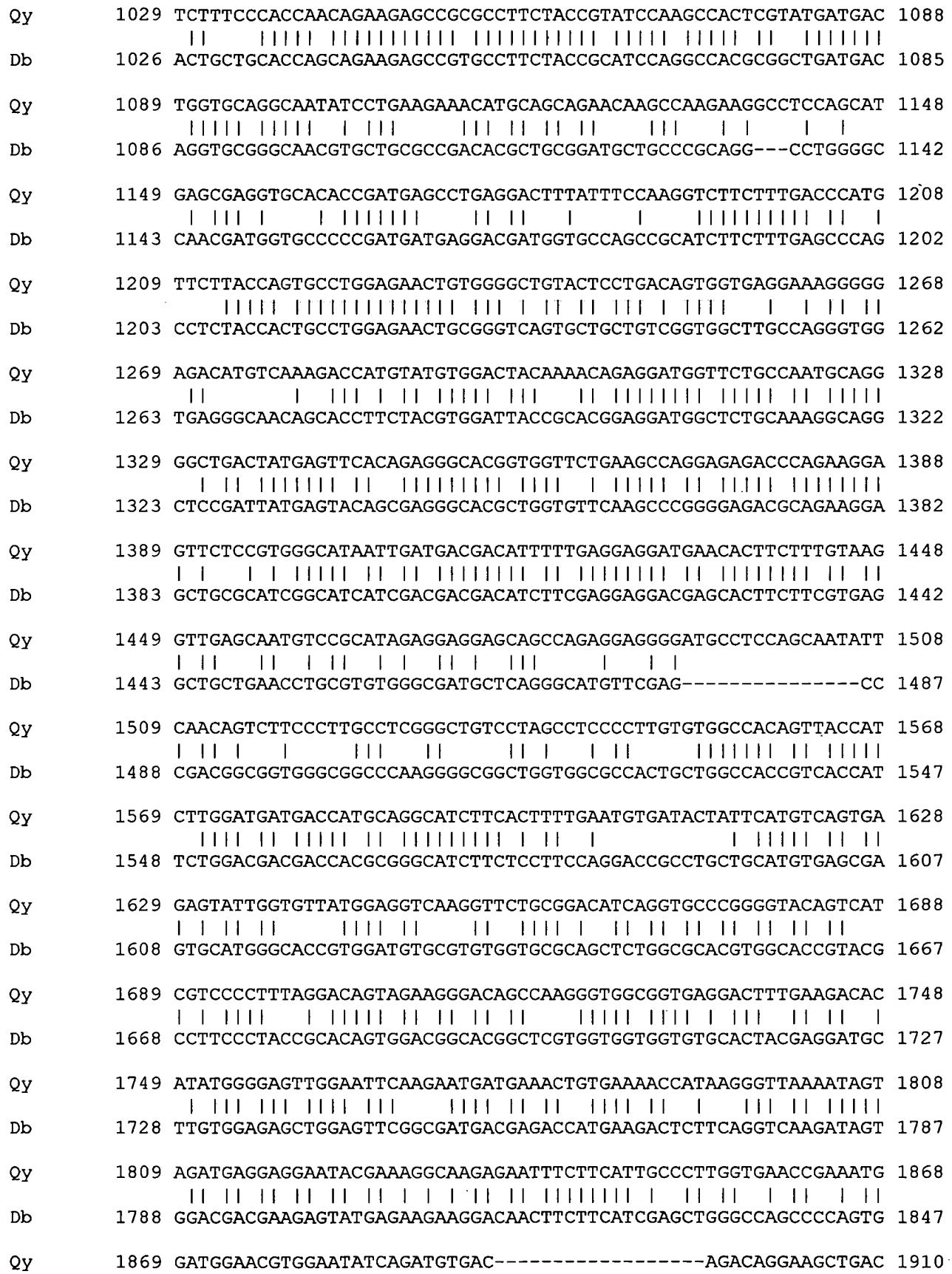

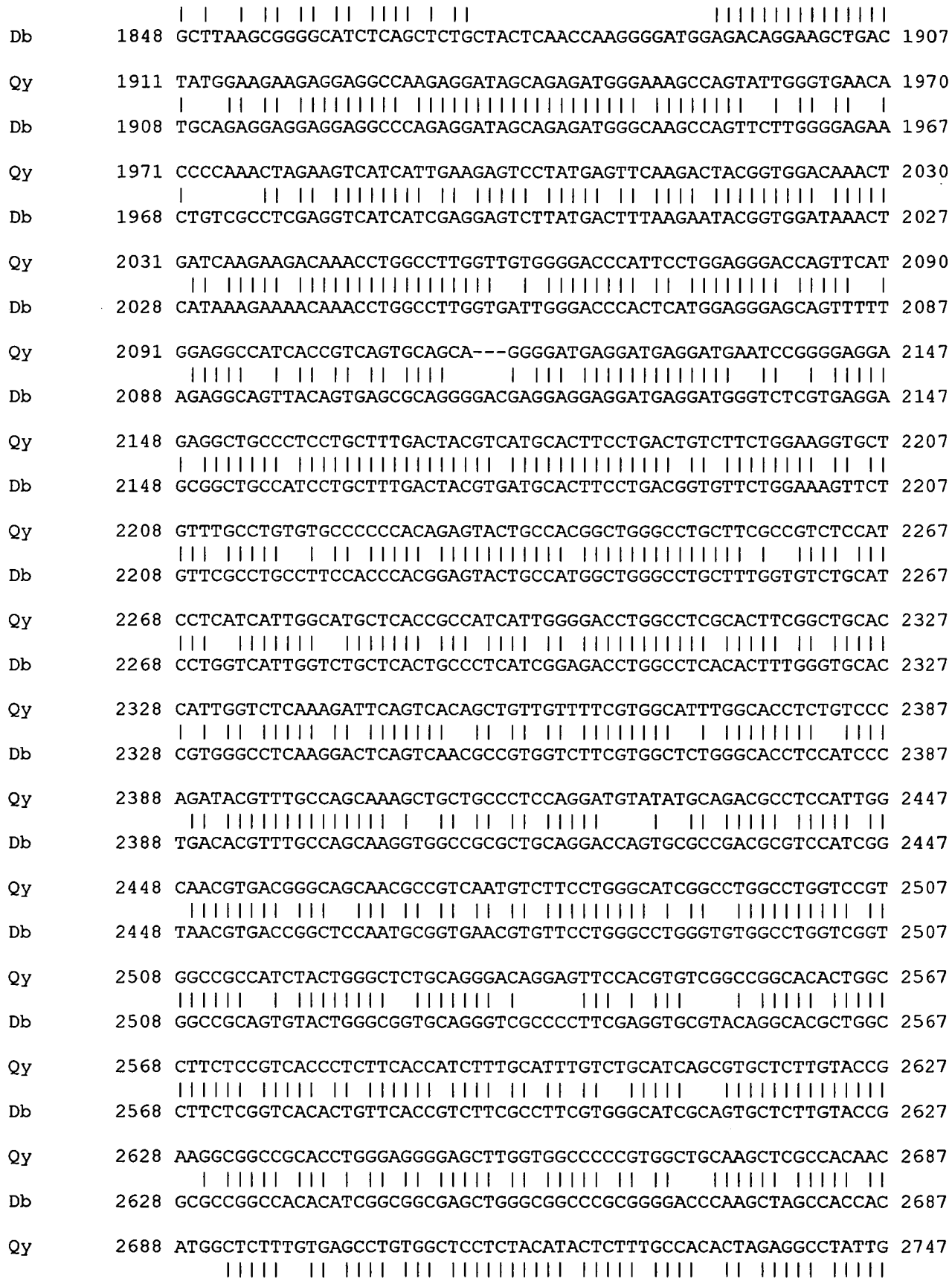

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Db       2688 CGCTCTCTTCCTGGGCCTCTGGTTCCTCTACATTCTCTTCGCCAGCCTGGAGGCTTATTG 2747

Qy       2748 CTACATCAAGGGGTTCTA 2765
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Db       2748 CCACATTCGGGGCTTCTA 2765
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RESULT 15
US-09-901-419-1
; Sequence 1, Application US/09901419
; Patent No. US20020069421A1
; GENERAL INFORMATION:
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: UMO1531.1
; CURRENT APPLICATION NUMBER: US/09/901,419
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/218,125
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4087
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (268)..(3180)
; NAME/KEY: sig_peptide
; LOCATION: (268)..(363)
; NAME/KEY: misc_feature
; LOCATION: (3178)
; OTHER INFORMATION: A Poly (H) affinity tag comprising 6 His residues
; OTHER INFORMATION: have been inserted at the C-Terminus end of the
; OTHER INFORMATION: coding region of the protein
US-09-901-419-1

Query Match 44.4%; Score 1227.8; DB 9; Length 4087;
Best Local Similarity 67.1%; Pred. No. 0;
Matches 1935; Conservative 0; Mismatches 777; Indels 171; Gaps 7;

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Qy         46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
              |||    || |  || | |||    || ||  |   | |   |   |     |||
Db        307 TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366

Qy        106 GGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAG 165
                 ||  ||  | |   |||  |  | | ||     ||| | || || |   |||| |||
Db        367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426

Qy        166 GAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
               |||| || ||  | || || ||| | ||  || |||||||| |||| ||||| |||||
Db        427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486

Qy        226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCT 285
              || |  | ||| |||||||||||| || | |||||||| ||||| || || |||||||||
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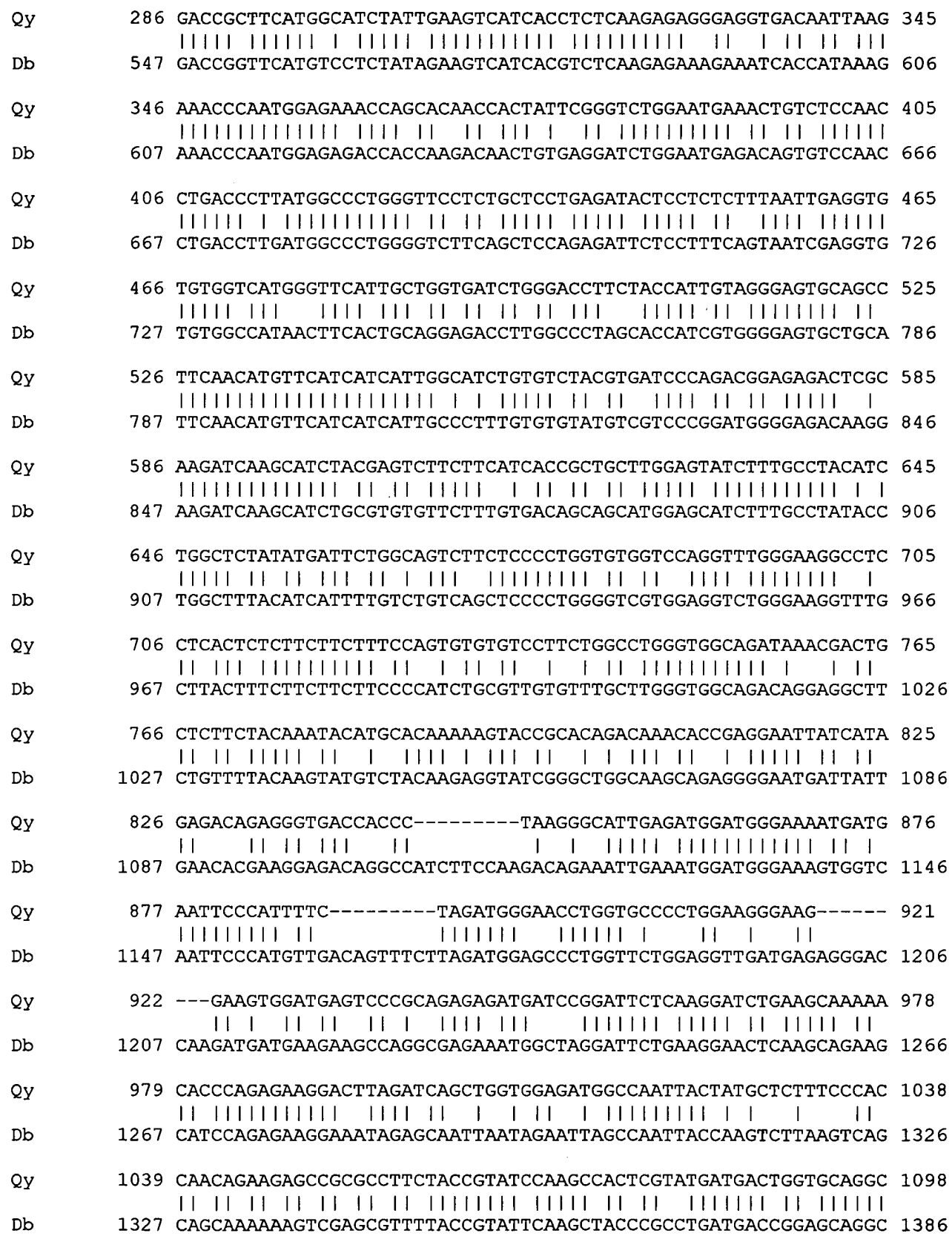

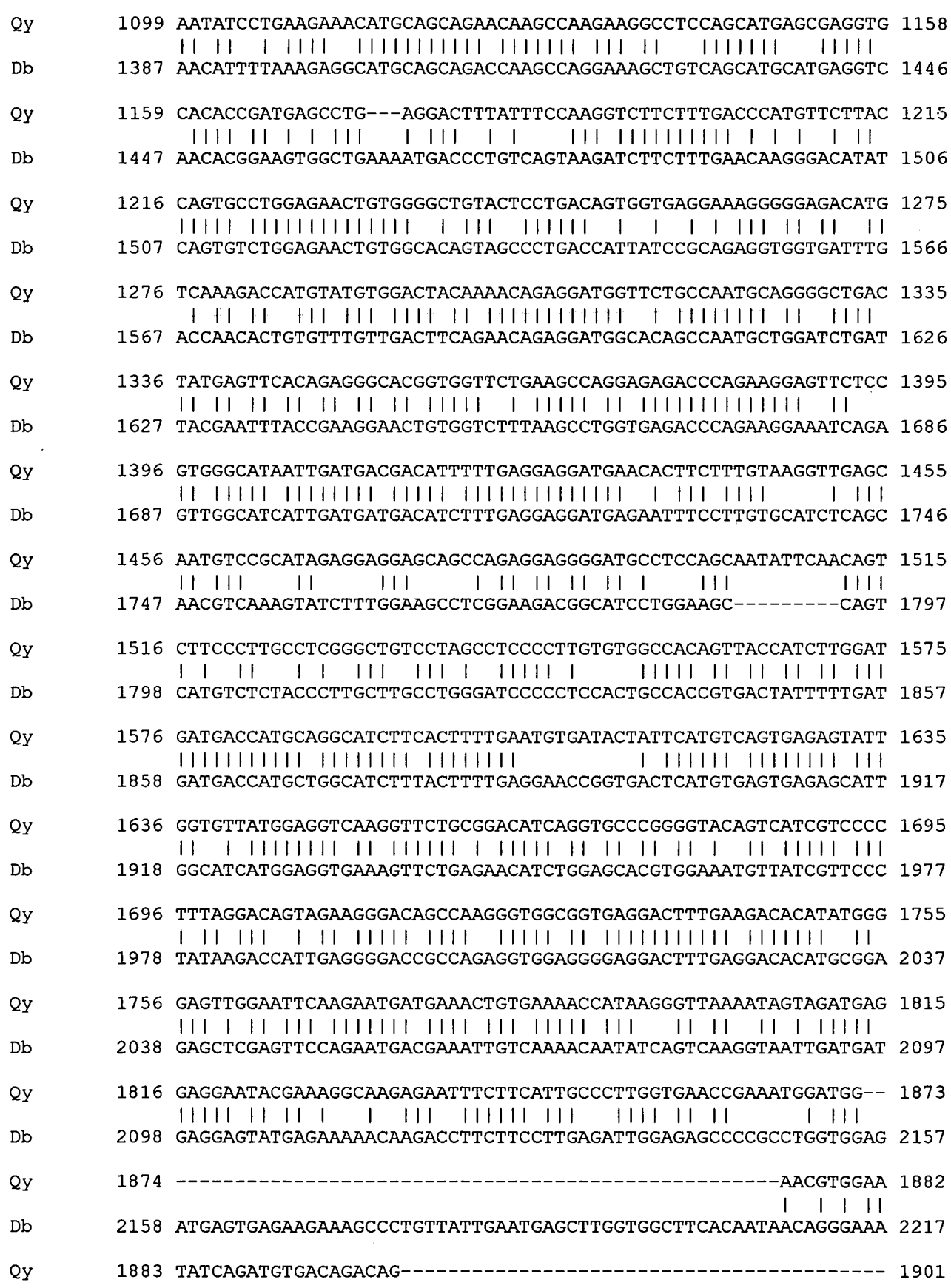

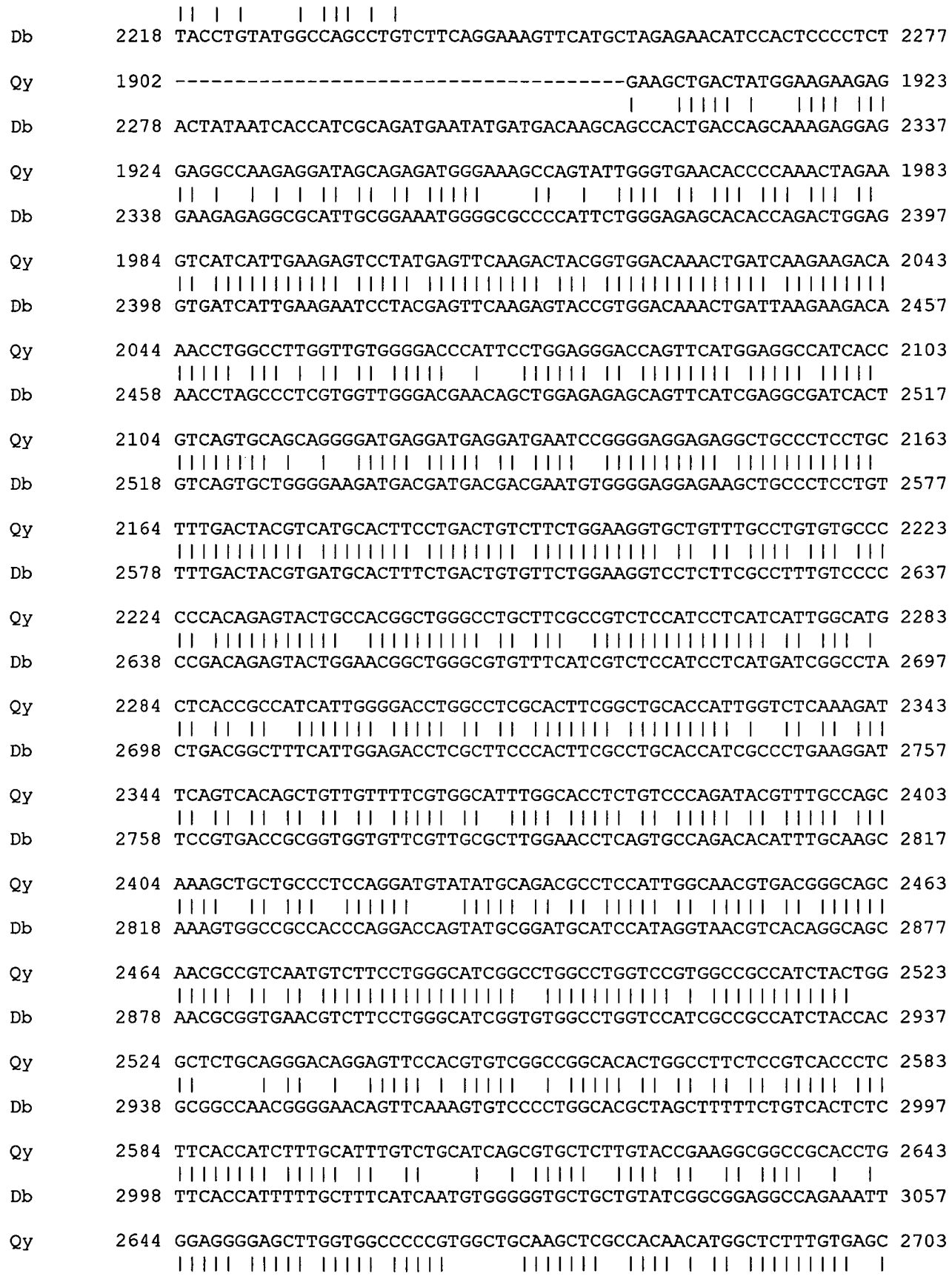

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Db       3058 GGAGGTGAGCTGGGTGGGCCCCGGACTGCCAAGCTCCTCACATCCTGCCTCTTTGTGCTC 3117

Qy       2704 CTGTGGCTCCTCTACATACTCTTTGCCACACTAGAGGCCTATTGCTACATCAAGGGGTTC 2763
              ||||||||| | |||||  ||||  || | || |||||||| ||| |||| || || |||
Db       3118 CTGTGGCTCTTGTACATTTTCTTCTCCTCCCTGGAGGCCTACTGCCACATAAAAGGCTTC 3177

Qy       2764 TAA 2766
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Db       3178 TAA 3180


Search completed: June 25, 2004, 16:08:42
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